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<120> Use of Computationally Derived Protein Structures of Genetic Polymorphisms in Pharmacogenomics for Drug Design and Clinical Applications

<141> 2000-11-10

<151> 1999-11-10

<151> 2000-11-01

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**BIBLIOGRAPHY**

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35          40          45
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100          105          110
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Arg	Gln	His	Leu	Leu	Arg 310	Trp	Gly	Phe	Thr	Thr 315	Pro	Asp	Lys	Lys	His 320		
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Val	Asn	Asp	Ile	Gln	Lys	Leu	Val 360	Gly	Lys	Leu	Asn	Trp 365	Ala	Ser	Gln		
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Ile	Tyr	Pro	Gly 370														

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ggg Gly	caa Gln	ata Ile	aag Lys 20	gaa Glu	gct Ala	yta Xaa	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp 30	gat Asp 30	aca Thr	gta Val	96
tta Leu	gaa Glu	gaa Glu 35	atg Met	aat Asn	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atw Xaa	ata Ile	ggg Gly	144
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	gta Val	ccc Pro	ata Ile	192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	caa Gln	aaa Lys 70	gct Ala	ata Ile	agt Ser	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aat Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	atg Met 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	cct Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	taa *	aag Lys	336
cca Pro	gga Gly	atg Met	gat Asp 115	ggc Gly	cca Pro	aga Arg	gtt Val	aaa Lys 120	caa Gln	tgg Trp	cca Pro	ttg Leu	aca Thr 125	gaa Glu	gaa Glu	384
aaa Lys	ata Ile	aaa Lys 130	gca Ala	tta Leu	gta Val	gaa Glu	atc Ile 135	tgt Cys	aca Thr	gaa Glu	atg Met	gaa Glu 140	aag Lys	gaa Glu	ggg Gly	432
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aga Arg	gaa Glu	ctt Leu	aat Asn	aag Lys 180	aaa Lys	act Thr	caa Gln	gac Asp	ttc Phe 185	tgg Trp	gaa Glu	gtt Val	caa Gln	tta Leu 190	gga Gly	576
ata Ile	cca Pro	cat His	ccc Pro 195	gca Ala	ggg Gly	cta Leu	aaa Lys	aag Lys 200	aaa Lys	aaa Lys	tca Ser	gta Val	aca Thr 205	gta Val	ctg Leu	624
gat Asp	gtg Val	ggt Gly 210	gat Asp	gca Ala	tat Tyr	ttt Phe	tca Ser 215	gtt Val	ccc Pro	tta Leu	gat Asp	aaa Lys 220	gaa Glu	ttc Phe	agg Arg	672
aag Lys	tat Tyr 225	act Thr	gca Ala	ttt Phe	acc Thr	ata Ile 230	cct Pro	agt Ser	aca Thr	aac Asn	aat Asn 235	gag Glu	aca Thr	cca Pro	ggg Gly	720
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gca Ala	ata Ile	ttc Phe	caa Gln	agt Ser 260	agc Ser	atg Met	aca Thr	aaa Lys	atc Ile 265	tta Leu	gag Glu	cct Pro	ttt Phe	aga Arg 270	aaa Lys	816

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Gly Gln Leu Lys Xaa Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
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Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val	
35 40 45	
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta ccc ata	192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile	
50 55 60	
gag atc tgt ggg cat aaa att ata ggt aca gta tta ata gga cct acc	240
Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gcc aac gta att gga aga aat ctg atg act cag ctt ggt tgc act	288
Pro Ala Asn Val Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr	

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		195				200						205																		
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Ala	Ile	Phe	Gln	Asp	Ser	Met	Thr	Lys	Ile	Leu	Asp	Pro	Phe	Arg	Lys															
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				325					330					335																
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1116

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 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
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 Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggt ttt atc aaa gta agg cag tat gat car ata ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
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 gag atc tgc ggg tat aaa gct gtg ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly Tyr Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80  
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 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
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 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140  
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 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
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 gcc ata aag aaa aaa gac ggt act aaa tgg aga aaa tta gta gat ttc 528  
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ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat caa gac ttc aga	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asp Phe Arg	
210 215 220	
aag tat act gca ttc act ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac atg gtt atc tat caa tat atg gat gat ttg tat gta	864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
ggc tct gac tta gaa aya ggg cag cat aga rca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
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Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag cta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
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att tat gca ggg	1116
Ile Tyr Ala Gly	
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ggg caa cta arg gaa gct cta ata gat aca gga gca gat gat aca gta Gly Gln Leu Xaa Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac ata gat ttg cca gga aga tgg aga cca aga atg ata ggg Leu Glu Asp Ile Asp Leu Pro Gly Arg Trp Arg Pro Arg Met Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aaa gta aag cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa ata tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct acg Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggg tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aag ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
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ata ccg cat ccc gca ggg tta ara aag aaa aga tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Xaa Lys Lys Arg Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gcc ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
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Gln Asn Pro Xaa Ile Val Ile Val Gln Tyr Val Asp Asp Leu Tyr Val				
	275	280	285	
ggg tct gac tta gaa ata ggg caa cat aga gca aaa ata gag gag ttg				912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu				
	290	295	300	
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Arg Glu His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Glu Lys His				
	305	310	315	320
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cac cct gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp				
	325		330	335
aaa tgg acc gta cag cct ata aat ttg cca gaa aaa gac agc tgg act				1056
Lys Trp Thr Val Gln Pro Ile Asn Leu Pro Glu Lys Asp Ser Trp Thr				
	340	345	350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag				1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln				
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Ile Tyr Ser Gly				
	370			
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly				
	1	5	10	15
ggg caa gta agg gaa gct cta tta gat aca gga gca gat gat aca gta				96
Gly Gln Val Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val				
	20	25	30	
tta gaa gaa atg aat ttg cca gga aaa tgg aag cca aaa atg ata ggg				144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly				
	35	40	45	
gga att ggg ggc ttt atc aaa gta aga cag tat gat caa ata ccc ata				192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile				
	50	55	60	
gaa atc tgt gga cat aaa gct ata ggg aca gtg tta ata gga cct aca				240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr				
	65	70	75	80
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act				288



Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	cct	att	agt	cct	att	gaa	act	gtg	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggg	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
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Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
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Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
145					150					155					160	
gcc	ata	aag	aaa	aaa	aac	agt	act	aga	tgg	agg	aaa	cta	gta	gac	ttc	528
Ala	Ile	Lys	Lys	Lys	Asn	Ser	Thr	Arg	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttt	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	gga	tta	aaa	aag	aga	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Arg	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aar	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aaa	tac	act	gca	ttc	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
225					230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctg	cca	caa	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
tca	ata	ttc	caa	agt	agy	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aag	816
Ser	Ile	Phe	Gln	Ser	Xaa	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gat	atc	tgt	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Asp	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	gca	aaa	ata				

gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gca agt cag	1104
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Ile Tyr Ala Gly	
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1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta kaa gaa atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Xaa Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta tcc wta	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Xaa	
50 55 60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tat aat act cca gta ttt	480
Lys Ile Ser Lys Ile ggg cct gaa aat cca tat aat act cca gta ttt	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttg gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	

aga gaa ctt aat aag aaa act caa gac ttc tgg gar gtt caa tta gga	576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca gga	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttt caa agy agc atg ata aga aty tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Xaa Ser Met Ile Arg Xaa Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gat tta gaa ata gaa cag cat aga gca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ala Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg tta agg tgg gga ttt acc aca cca gay aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp	
325 330 335	
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag ttr gtg gga aaa ttr aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Xaa Val Gly Lys Xaa Asn Trp Ala Ser Gln	
355 360 365	
att tac tca ggg	1116
Ile Tyr Ser Gly	
370	

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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
275				280				285								
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	rca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Xaa	Lys	Ile	Glu	Glu	Leu	
290				295				300								
agg	caa	cat	ctg	ttg	aag	tgg	gga	ttt	acc	aca	cca	gac	aaa	aaa	cat	960
Arg	Gln	His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	
305				310				315				320				
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggt	tat	gaa	ctc	cat	cca	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325				330				335				
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	caa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Gln	Lys	Asp	Ser	Trp	Thr	
				340				345				350				
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
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Ile	Tyr	Pro	Gly													
370																

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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Xaa	Val	Thr	Ile	Lys	Val	Gly	
1				5					10					15		
ggg caa cta aag gaa gcc cta ata gat aca gga gca gat gat aca gtg																96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Ile	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg																144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Leu	Ile	Gly	
		35					40					45				
gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata																192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Xaa	Pro	Ile	
	50					55					60					
gaa atc tgt gga cat aaa gct gta ggt tca gtg tta gta gga cct aca																240
Glu	Ile	Cys	Gly	His	Lys	Ala	Val	Gly	Ser	Val	Leu	Val	Gly	Pro	Thr	
65					70				75						80	
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[illegible]

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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggt	cca	aaa	gtt	aaa	caa	tgg	cca	tta	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgc	aca	gaa	ttg	gaa	aag	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Leu	Glu	Lys	Glu	Gly	
	130					135					140					
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Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
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gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	cct	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggt	gat	gca	tat	ttt	tca	ata	ccc	tta	gat	gaa	gaa	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Ile	Pro	Leu	Asp	Glu	Glu	Phe	Arg	
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Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Pro	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
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Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
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gaa	aat	cca	gat	ata	gtt	atc	tac	caa	tac	atg	gat	gac	tta	tat	gta	864
Glu	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gat	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
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Arg	Gln	Tyr	Leu	Trp	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
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Gln	Gln	Glu	Pro	Pro	Phe	Arg	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325				330						335		
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
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ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt atg aac aat gag aca cca gga	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Met Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca atg gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agt atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
cag aat cca gac ata gtc atc tat caa tac atg gat gat tta tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tcg gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ttg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
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Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
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325 330 335	
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340 345 350	
gtt aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt caa	1104
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ggg caa cta aag gag gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac ata gat ttg cca gga agr tgg aaa cca aaa atg ata ggg Leu Glu Asp Ile Asp Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa ata tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cgg att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Arg Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtg caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aar gay ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gcc ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc cta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270 275 280 285 290 295 300	816

	260	265	270	
caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta				864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val				
	275	280	285	
ggg tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg				912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu				
	290	295	300	
aga gaa cat ctg ttg agg tgg gga ttt acc acc cca gac aaa aaa cat				960
Arg Glu His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His				
	305	310	315	320
cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp				
	325	330	335	
aaa tgg acc gtr cag cct ata gag ctg cca gaa aaa gac agc tgg act				1056
Lys Trp Thr Xaa Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr				
	340	345	350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag				1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln				
	355	360	365	
att tac cca ggg				1116
Ile Tyr Pro Gly				
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly				
	1	5	10	15
ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta				96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val				
	20	25	30	
tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg				144
Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly				
	35	40	45	
gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata				192
Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile				
	50	55	60	
gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca				240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr				
	65	70	75	80
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act				288

Pro	Ala	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aga	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Arg	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	aca	gaa	atc	tgt	wca	gag	atg	gaa	aag	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Thr	Glu	Ile	Cys	Xaa	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aac	act	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcy	ata	cac	aag	aaa	aat	agt	aat	aga	tgg	aga	aaa	gta	gta	gat	ttc	528
Xaa	Ile	His	Lys	Lys	Asn	Ser	Asn	Arg	Trp	Arg	Lys	Val	Val	Asp	Phe	
				165					170					175		
agg	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	gga	tta	aaa	aag	aac	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aag	gat	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210				215						220					
aag	tat	act	gcg	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
atc	aga	tac	cag	tac	aat	gtg	ctt	cca	caa	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aga	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Arg	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gaa	ata	gtt	atc	tgt	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Glu	Ile	Val	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	aak	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Xaa	Glu	Leu	
	290					295					300					
aga	saa	cat	ctg	ttg	agg	tgg	gga	ttt	ttc	aca	cca	gac	caa	aaa	cat	960
Arg	Xaa	His	Leu	Leu	Arg	Trp	Gly	Phe	Phe	Thr	Pro	Asp	Gln	Lys	His	
	305				310					315					320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aar	gac	agt	tgg	acw	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Xaa	
			340					345					350			



gty aat gac ata cag aaa tta gtk gga aaa ttg aat tgg gca agt caa	1104
Xaa Asn Asp Ile Gln Lys Leu Xaa Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tac cca ggg	1116
Ile Tyr Pro Gly	
370	
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<223> Portion of HIV Reverse Transcriptase	
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg	144
Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly	
35 40 45	
gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta aca gaa atc tgt wca gag atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Xaa Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcy ata cac aag aaa aat agt aat aga tgg aga aaa gta gta gat ttc	528
Xaa Ile His Lys Lys Asn Ser Asn Arg Trp Arg Lys Val Val Asp Phe	
165 170 175	

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca gga tta aaa aag aac aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gat ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gcg ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
atc aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aga atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata aak gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Xaa Glu Leu	
290 295 300	
aga saa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat	960
Arg Xaa His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agt tgg acw	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Xaa	
340 345 350	
gty aat gac ata cag aaa tta gtk gga aaa ttg aat tgg gca agt caa	1104
Xaa Asn Asp Ile Gln Lys Leu Xaa Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tac cca ggg	1116
Ile Tyr Pro Gly	
370	

<210> 25  
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 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

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ggg caa cta aag gaa gct cta cta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg agt ttg cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta tcc atg Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Met 50 55 60	192
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga tct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Ser Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ytg ttg act cag ctt ggg tgc act Pro Val Asn Ile Ile Gly Arg Asn Xaa Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gar ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aaa act caa gat ttc tgg gaa rtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Xaa Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta caa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Gln Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtc ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tat agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Tyr Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816

260	265	270			
caa aat cca gac ata gtt atc tac caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	275	280	285	864	
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	290	295	300	912	
aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	305	310	315	320	960
cag aaa gaa cct cca ttc ctc tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	325	330	335	1008	
aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	340	345	350	1056	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	355	360	365	1104	
att tac cca ggg Ile Tyr Pro Gly	370			1116	
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ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	20	25	30		96
tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly	35	40	45		144
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile	50	55	60		192
gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr	65	70	75	80	240
cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act					288





gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga ata	576
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile	
180 185 190	
cca cat ccc gca ggg tta aaa aag aac aag tca gta aca att ctg gat	624
Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Ile Leu Asp	
195 200 205	
gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gaa ttc agg aag	672
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg Lys	
210 215 220	
tat act gca ttt acc ata cct agt ata aat aat gag aca cca ggg att	720
Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile	
225 230 235 240	
aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca gca	768
Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala	
245 250 255	
ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa caa	816
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln	
260 265 270	
aat cca gac ata gtt atc tat cag tac gtg gat gat ttg tat gta gga	864
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly	
275 280 285	
tct gat tta gaa ata ggg gag cat aga aca aaa ata gag gaa ctg aga	912
Ser Asp Leu Glu Ile Gly Glu His Arg Thr Lys Ile Glu Glu Leu Arg	
290 295 300	
car cat ctg tta arg tgg gga ttt ttc aca cca gaa caa aaa cat cag	960
Gln His Leu Leu Xaa Trp Gly Phe Phe Thr Pro Glu Gln Lys His Gln	
305 310 315 320	
aaa gaa cct ccm ttc cak tgg atg ggt tat gaa ctc cay cct gat aaa	1008
Lys Glu Pro Xaa Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp Lys	
325 330 335	
tgg aca gta cas cct ata gtg ctg cca gaa aaa gat agc tgg act gtc	1056
Trp Thr Val Xaa Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val	
340 345 350	
aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag att	1104
Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile	
355 360 365	
tac cca ggg	1113
Tyr Pro Gly	
370	

<210> 28  
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 <222> (0)...(297)  
 <223> HIV Protease  
  
 <221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

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ggg caa ata aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Ile Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val 35 40 45	144
gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct atk gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Xaa Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu 115 120 125	384
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aaa att aca aaa att ggg cct gaa aat ccg tac aat act cca ata ttt Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
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gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104  
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ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
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tta gaa gaa atg agc tta cca gga aga tgg aaa cca aaa atg ata ggg 144  
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                   35                          40                          45

gga att gga ggk ttt atc aaa gtg agm cag tat gat cag ata ctc ata 192  
 Gly Ile Gly Xaa Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Leu Ile  
                   50                          55                          60

gaa aty tgt gga cat aaa gct ata ggt aca gtr tta ata gga cct aca 240  
 Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr  
   65                          70                          75                          80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
                   85                          90                          95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aaa 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                   100                          105                          110

cca gga atg gat ggc cca aaa gtc aaa caa tgg cca ttg aca gaa gaa 384  
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 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Xaa  
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aaa att aca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
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gcc ata aag aag aaa aac agt gat aaa tgg aga aaa tta gta gat ttc 528  
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ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
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cta gaa gac gtg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Val His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
          35           40           45

gga att gga ggt ttt atc aaa gta aga cag tat gat gag gta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Glu Val Pro Ile
  50           55           60

gaa ctc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Leu Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
  65           70           75           80

ccc gtc aac ata att gga aga aat ctg wtg act caa ctt ggg tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Leu Gly Cys Thr
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cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
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Lys Ile Ser Arg Val Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
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gyc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
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Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Xaa
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Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
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Lys Tyr Thr Ala Phe Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
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Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys

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09709905-11000

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Gly Gln Leu Lys Glu Ala Leu Leu Xaa Thr Gly Ala Asp Asp Thr Xaa	
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tta gaa gac atg act ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Asp Met Thr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
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Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Glu Ile Pro Ile	
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gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
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Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aaa	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
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Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca ttw gta gaa att tgt gca gaa ctg gaa aag gaa ggg	432
Lys Ile Lys Ala Xaa Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly	
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Gly Gln Leu Lys Glu Ala Leu Xaa Asp Thr Gly Ala Asp Asp Thr Val	
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Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly	
35 40 45	
gga att gga ggt ttt att aaa gta aaa cag tat gaa cag ata acc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Thr Ile	
50 55 60	
gam atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca	240
Xaa Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr	
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cct gtc aac gta att gga aga aat atg atg act cag att ggt tgc act	288
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Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg	
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Lys Tyr Thr Ala Phe Thr Ile Pro Arg Tyr Asn Asn Glu Thr Pro Gly	
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Thr Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro	
245 250 255	
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Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Arg	

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Gln Asn Pro Asp Ile Val Ile Tyr	Gln Tyr Val Asp Asp Leu Tyr Val		
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Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu			
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Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His			
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			
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gga att gga ggt ttt atc aar gta aaa cag tat gat cag ata ccc ata			192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile			
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gaa atc tgt ggg cat aaa gct ata ggt aca gta tta gta gga cct aca			240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr			
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cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act			288

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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
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Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
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Glu Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr	
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Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ctg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt gca gaa ttg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly	
130 135 140	
aag att tca aaa att ggg ccy gaa aat cca tac aay act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Xaa Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aar aac agt act ara tgg aga aaa kta gta gat ttc	528
Ala Ile Lys Lys Lys Asn Ser Thr Xaa Trp Arg Lys Xaa Val Asp Phe	
165 170 175	

09709905-11000

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aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
      180                      185                      190

ata cca cat ccc gca ggg cta aag aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
      195                      200                      205

gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat gaa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
      210                      215                      220

aag tat aca gcc ttt acc tat act ggt tcc aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Tyr Thr Gly Ser Asn Asn Glu Thr Pro Gly
      225                      230                      235                      240

att aga tat car tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
      245                      250                      255

gca ata ttc caa agc agc atg aca aaa gtc tta gaa cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Val Leu Glu Pro Phe Arg Lys
      260                      265                      270

caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
      275                      280                      285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
      290                      295                      300

aga caa cat ctg tta agg tgg gga ttt tac aca cca gac gaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Glu Lys His
      305                      310                      315                      320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gac      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
      340                      345                      350

gtt aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gcc agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tac cca ggg
Ile Tyr Pro Gly
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<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

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<221> CDS
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<223> Portion of HIV Reverse Transcriptase

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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg atg aca cag ctt ggt tgt act Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Ile Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta ggg Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca gga tta aaa aag aat aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gat cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys	816

	260	265	270	
cag aat cca gat ata gtt atc tat caa tac atg gat gat ttg tat gta				864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val				
	275	280	285	
gga tct gac tta gag ata ggg cag cat aga gca aaa ata gag gaa ctg				912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu				
	290	295	300	
aga gca cat ctg ttg aag tgg gga ttt acc acc cca gac aaa aaa cat				960
Arg Ala His Leu Leu Lys Trp Gly Phe Thr Pro Asp Lys Lys His				
	305	310	315	320
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp				
	325	330	335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act				1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr				
	340	345	350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag				1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln				
	355	360	365	
att tac gca ggg				1116
Ile Tyr Ala Gly				
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<223> Portion of HIV Reverse Transcriptase				
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	1	5	10	15
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca ata				96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile				
	20	25	30	
tta gaa gac aya rat ttg cca ggg aga tgg aaa cca aaa ata ata ggg				144
Leu Glu Asp Xaa Xaa Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly				
	35	40	45	
gga att gga ggt ttt atc aga gta aga cag tat gat cag gta ccc ata				192
Gly Ile Gly Gly Phe Ile Arg Val Arg Gln Tyr Asp Gln Val Pro Ile				
	50	55	60	
gaa atc tgt gga cat aaa gtt gta agt aca gta tta gta gga cct aca				240
Glu Ile Cys Gly His Lys Val Val Ser Thr Val Leu Val Gly Pro Thr				
	65	70	75	80
cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act				288



Pro	Ala	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Met	Thr	Gln	Ile	Gly	Cys	Thr		
				85					90					95			
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336	
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
			100					105					110				
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384	
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
		115					120					125					
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	gaa	gaa	ttg	gaa	aag	gat	ggg	432	
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Glu	Glu	Leu	Glu	Lys	Asp	Gly		
	130					135					140						
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480	
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
	145				150					155					160		
gcc	ata	aag	aaa	aag	aac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528	
Ala	Ile	Lys	Lys	Lys	Asn	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe		
				165					170					175			
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576	
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
			180					185					190				
ata	cca	cat	cct	gca	gga	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624	
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu		
		195					200					205					
gat	gtg	ggg	gat	gca	tat	ttt	tca	att	ccc	tta	gat	gaa	gac	ttc	aga	672	
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Ile	Pro	Leu	Asp	Glu	Asp	Phe	Arg		
	210					215					220						
aag	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720	
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly		
	225				230					235					240		
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768	
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro		
			245						250					255			
tca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816	
Ser	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys		
			260					265					270				
caa	aat	cca	gac	ata	gtc	atc	tat	caa	tat	atg	gat	gat	ttg	tat	gta	864	
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val		
		275					280					285					
gga	tct	gac	tta	gag	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912	
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu		
	290					295					300						
aga	cag	cat	ctg	tgg	aag	tgg	ggg	ttt	tac	aca	cca	gac	ara	aaa	cat	960	
Arg	Gln	His	Leu	Trp	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Xaa	Lys	His		
	305				310				315					320			
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gac	1008	
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
			325						330					335			
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aag	gac	agc	tgg	act	1056	
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr		
			340					345					350				



aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtc caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cct gca ggg tta aaa aag aac aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat raa gat tca gra	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Xaa Asp Ser Xaa	
210 215 220	
agt aca ctg cat tta cca tac cta gta cgr acc aat gag aca cca ggg	720
Ser Thr Leu His Leu Pro Tyr Leu Val Xaa Thr Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac tta gtt atc tgt caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Leu Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gat tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat	960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc cgt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta caa gcc tat aaa gct gcc aga aaa aga cag ctg gac	1056
Lys Trp Thr Val Gln Ala Tyr Lys Ala Ala Arg Lys Arg Gln Leu Asp	
340 345 350	
tgt caa tga cat tac mag aaa gtt agt ggg gaa aat tgg aat ttg ggg	1104
Cys Gln * His Tyr Xaa Lys Val Ser Gly Glu Asn Trp Asn Leu Gly	
355 360 365	
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Gln Gly Gln Ile Tyr Cys Gln Gly	
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 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1120)  
 <223> Portion of HIV Reverse Transcriptase







gtc  
Val

1059

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1 5 10 15  
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
20 25 30  
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
35 40 45  
gga att gga ggt ttt atm aaa gta aga cag tat gat cag ata cyc ata 192  
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile  
50 55 60  
gaa atc tgt gga yat aaa gct ata ggt acr gta tta gta gga ccc acg 240  
Glu Ile Cys Gly Xaa Lys Ala Ile Gly Xaa Val Leu Val Gly Pro Thr  
65 70 75 80  
cct gtc aac rta att gga aga aat ctg wtg act cag att ggt tgc act 288  
Pro Val Asn Xaa Ile Gly Arg Asn Leu Xaa Thr Gln Ile Gly Cys Thr  
85 90 95  
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
100 105 110  
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
115 120 125  
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432  
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
130 135 140  
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
145 150 155 160  
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttr gta gat ttc 528  
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Xaa Val Asp Phe  
165 170 175  
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtc caa tta gga 576  
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
180 185 190





35					40					45						
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Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile	
	50					55					60					
gaa	aty	tgt	ggg	cat	aaa	gct	ata	ggt	aca	gta	tta	gta	ggg	cct	aca	240
Glu	Xaa	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
	65				70				75						80	
cct	gtc	aac	ata	att	gga	aga	aat	ttg	ttg	act	cag	att	ggt	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85				90					95			
tta	aat	ttt	cct	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	ccc	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	atg	gaa	aaa	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
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Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aag	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttt	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	ccg	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aag	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu		
		195				200					205					
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aaa	tat	ast	gca	ttt	acc	ata	ccg	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Xaa	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	ccg	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245				250						255		
gca	ata	ttc	caa	tgt	agc	atg	aca	aaa	atc	tta	gaa	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280				285					
gga	tct	gac	ttg	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	cag	cat	ctg	ttg	aaa	tgg	ggr	ttt	acc	aca	cca	gac	aag	aaa	cat	960

Arg	Gln	His	Leu	Leu	Lys	Trp	Xaa	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	
305					310					315					320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gta	caa	ccg	ata	gag	ctg	cca	gaa	aaa	gaa	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Glu	Leu	Pro	Glu	Lys	Glu	Ser	Trp	Thr	
			340					345					350			
gtc	aat	gac	ata	cag	aag	tta	gtg	gg								1082
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val									
		355					360									

<210> 44  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease  
  
 <221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 44																	
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Ile	Val	Thr	Val	Lys	Ile	Gly		
1				5					10					15			
ggg	caa	cta	aag	gaa	gct	yta	tta	gat	aca	gga	gca	gat	gat	aca	gta		96
Gly	Gln	Leu	Lys	Glu	Ala	Xaa	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val		
			20					25					30				
tta	gaa	gaa	atg	aat	tta	cca	gga	aaa	tgg	aaa	cca	aaa	ata	ata	ggg		144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Lys	Trp	Lys	Pro	Lys	Ile	Ile	Gly		
		35					40					45					
gga	att	gga	ggt	ttt	gcc	aaa	gta	aga	cag	tat	gat	cag	ata	ccc	ata		192
Gly	Ile	Gly	Gly	Phe	Ala	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile		
	50					55					60						
gaa	atc	tka	gga	cat	aaa	gtt	ata	ggt	aca	gtc	tta	gta	gga	cct	aca		240
Glu	Ile	Xaa	Gly	His	Lys	Val	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr		
	65				70					75					80		
cct	gcc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	att	ggt	tgc	act		288
Pro	Ala	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr		
				85					90					95			
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag		336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
			100					105					110				
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa		384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
		115					120					125					
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga		432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly		
	130					135					140						



**BOOK REVIEW**

<400> 45

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Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Ser	Ile		
	50					55					60						
gaa	atc	tgt	gga	cat	aaa	gct	ata	ggg	aca	gta	tta	gta	gga	cct	aca	240	
Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	80	
65					70				75								
cct	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	att	ggg	tgc	act	288	
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	95	
				85				90									
tta	aat	ttt	cct	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336	
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	110	
			100					105									
cca	gga	atg	gac	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384	
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	125	
		115					120					125					
aaa	ata	aaa	gca	tta	gta	gag	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga	432	
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	140	
	130					135											
aaa	att	tca	aaa	att	ggg	cct	gaa	aac	cca	tac	aat	act	cca	gta	ttt	480	
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	160	
	145				150					155							
gcc	ata	aag	aaa	aaa	gac	agt	act	aag	tgg	aga	aaa	tta	gta	gat	ttc	528	
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	175	
				165					170								
aga	gaa	ctt	aat	aaa	aga	act	caa	gac	ttc	tgg	gag	gtt	caa	tta	gga	576	
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	190	
			180					185									
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	cta	624	
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	205	
		195					200										
gat	gtg	ggc	gat	gca	tat	ttc	tca	gtt	ccc	tta	gat	gaa	gac	ttc	aga	672	
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	220	
	210					215											
aaa	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720	
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	240	
	225				230					235							
act	aga	tat	cag	tac	aat	gtg	ctc	cca	cag	gga	tgg	aaa	gga	tca	cca	768	
Thr	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	255	
				245					250								
gca	ata	ttc	caa	tgt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816	
Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	270	
			260					265									
caa	aat	cca	gac	cta	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864	
Gln	Asn	Pro	Asp	Leu	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	285	
		275					280										
gga	tct	gac	tta	gaa	ata	gga	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912	
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	300	
	290					295											
aga	caa	cat	ctg	ttg	agg	tgg	gga	ttt	acc	acc	cca	gac	aaa	aaa	cat	960	
Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	320	
	305				310					315							







<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1115)  
 <223> Portion of HIV Reverse Transcriptase

<400> 48  
 cct cag atc act ctt tgg caa cga ccc ctc gtc aca gta aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly  
 1 5 10 15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

ata gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
 Ile Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aaa cag tat gag cag gta ccc ata 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Val Pro Ile  
 50 55 60

gaa ctc tgt ggg cgt aaa act ata ggt aca gta tta gta gga cct aca 240  
 Glu Leu Cys Gly Arg Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aac ctg atg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

gcy ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat cct gca ggg tta aaa aag aag aaa tca gta aca gta ttg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccg tta gat aaa gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg  
 210 215 220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720

[illegible]

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<210> 49
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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gga Gly	att Ile 50	gga Gly	ggt Gly	ttc Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	ata Ile	ccc Pro	ata Ile	192
gaa Glu 65	atc Ile	tgt Cys	ggc Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	cta Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aag Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	atc Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	ggg Gly	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu 180	aat Asn	aag Lys	aaa Lys	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	cct Pro	gca Ala	ggg Gly	tta Leu 200	aaa Lys	aag Lys	aam Xaa	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gaa Glu	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	acc Thr	gca Ala	ttt Phe	cca Pro 230	tcc Ser	cta Leu	gtt Val	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	gga Gly 240	720
atc Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttt Phe	caa Gln	agt Ser	agc Ser	atg Met	aca Thr 265	aaa Lys	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	gta Val	gag Glu	gag Glu	ctg Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960

cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro 325 Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr 340 Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agc cag	1104
Val Asn Asp 355 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 365	
att tac cca ggg	1116
Ile Tyr Pro Gly 370	
<210> 50	
<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0) ... (297)	
<223> HIV Protease	
<221> CDS	
<222> (298) ... (1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 50	
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Asn Ile Lys Ile Gly 1 5 10 15	
gga caa ctg aag gaa gct cta ttg gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45	
gga att gga ggt ttk gtc aaa gta aga cag tat gat cag ata cct gta	192
Gly Ile Gly Gly Xaa Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Val 50 55 60	
gaa att tgt gga cat aaa gyt ata ggt aca gtc tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Xaa Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	
cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	

130	135	140	
aaa att tca aag att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160			480
gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta mam aag aac aaa tca gta aca gtg cta Ile Pro His Pro Ala Gly Leu Xaa Lys Asn Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg 210 215 220			672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tay aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc cag agt agc atg aca aga atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gaa ata gtc atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285			864
gca tct gac tta gaa ata gag aaa cat aga aca aaa ata gag gaa ctg Ala Ser Asp Leu Glu Ile Glu Lys His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tat gga ggg Ile Tyr Gly Gly 370			1116

&lt;210&gt; 51

&lt;211&gt; 1116

&lt;212&gt; DNA

&lt;213&gt; Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

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 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg 48  
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly  
 1 5 10 15  
 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30  
 tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly  
 35 40 45  
 gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata cct ata 192  
 Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60  
 gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr  
 65 70 75 80  
 cct gcc aac ata att gga aga gat ctg ttg act cag att ggt tgc act 288  
 Pro Ala Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95  
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly  
 130 135 140  
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cct gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gcc ata aag aaa aaa aac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175  
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190  
 ata cca cat ccc gcg ggg tta aaa aag aaa aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205  
 gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg  
 210 215 220  
 aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg 720

000111" 50660450

Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
225					230					235					240	
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Val	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
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gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	ccc	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
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caa	aat	cca	gac	ata	gtt	atc	tat	caa	tat	gtg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
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Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Ala	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	caa	cat	ctg	tgg	agg	tgg	ggg	ttt	tac	aca	cca	gac	aaa	aaa	cat	960
Arg	Gln	His	Leu	Trp	Arg	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
	305				310					315					320	
cag	aaa	gaa	ccc	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
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aaa	tgg	aca	gta	caa	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
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gtc	aat	gac	ata	cag	aaa	tta	gtg	ggg	aaa	ttg	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
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Ile	Tyr	Ala	Gly													
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Thr	Ile	Lys	Xaa	Gly	
	1			5					10					15		
ggg	caa	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atr	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Xaa	Ile	Gly	
		35					40					45				

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ycc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt tca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata aty gga aga aat ctg atg act cag att ggt tgc act Pro Val Asn Ile Xaa Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa ack gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Xaa Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gra gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Xaa Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
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gcc ata aag aaa aag aat agt act aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aac aaa tca gtg aca gta ytg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Xaa 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt atr aac aat gag aaa cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Xaa Asn Asn Glu Lys Pro Gly 225 230 235 240	720
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car aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ttg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tta agg tgg gga ttt ttc aca cca gaa caa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His 305 310 315 320	960



cag aaa gaa ccg cca ttc ctt tgg atg ggt tat gaa cta cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg acg gta cag cct ata aag ctg cca gaa aaa gat agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
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att tay gca ggg	1116
Ile Tyr Ala Gly	
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1 5 10 15	
ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gtg aga cag tat gat cag rta ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile	
50 55 60	
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga tct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
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Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	

00011-50660460

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aga gaa ctt aat aag Arg Glu Leu Asn Lys 180	aaa act caa gac ttc Lys Thr Gln Asp Phe 185	tgg gaa gtt caa tta gga Trp Glu Val Gln Leu Gly 190	576
atc cca cat cct gca Ile Pro His Pro Ala 195	ggg tta aaa aag Gly Leu Lys Lys 200	aaa tca gta aca gta ctg Lys Lys Lys Ser Val Thr Val 205	624
gat gtg ggt gat gca Asp Val Gly Asp Ala 210	tat ttt tca gtt ccc Tyr Phe Ser Val Pro 215	tta gat aaa gac ttc cgg Leu Asp Lys Asp Phe Arg 220	672
aag tat act gca ttt Lys Tyr Thr Ala Phe 225	acc ata cct agt aca Thr Ile Pro Ser Thr 230	aac aat gag aca cca gga Asn Asn Glu Thr Pro Gly 235	720
att aga tat cag tac Ile Arg Tyr Gln Tyr 245	aat gtg ctt cca caa Asn Val Leu Pro Gln 250	gga tgg aaa gga tca cca Gly Trp Lys Gly Ser Pro 255	768
gca ata ttc caa agt Ala Ile Phe Gln Ser 260	agc atg aca aaa atc Ser Met Thr Lys Ile 265	tta gag cct ttt agg aat Leu Glu Pro Phe Arg Asn 270	816
aaa aat cca gac ata Lys Asn Pro Asp Ile 275	gtt atc tat caa tac Val Ile Tyr Gln Tyr 280	gtg gat gat ttg tat gta Val Asp Asp Leu Tyr Val 285	864
gga tct gac cta gaa Gly Ser Asp Leu Glu 290	ata ggg cag cat aga Ile Gly Gln His Arg 295	gca aaa ata gag gaa ctg Ala Lys Ile Glu Glu Leu 300	912
aga gaa cat ctg ttg Arg Glu His Leu Leu 305	aag tgg ggg ttt act Lys Trp Gly Phe Thr 310	aca cca gac aaa aaa cat Thr Pro Asp Lys Lys His 315	960
cag aaa gaa cct cca Gln Lys Glu Pro Pro 325	ttc ctt tgg atg ggt Phe Leu Trp Met Gly 330	tat gaa ctc cat cct gat Tyr Glu Leu His Pro Asp 335	1008
aaa tgg aca gtc cag Lys Trp Thr Val Gln 340	cct ata gag ctg cca Pro Ile Glu Leu Pro 345	gaa aaa gac agc tgg act Glu Lys Asp Ser Trp Thr 350	1056
gtc aat gac ata cag Val Asn Asp Ile Gln 355	aag tta gtg gga aaa Lys Leu Val Gly Lys 360	ttg aat tgg gca agt cag Leu Asn Trp Ala Ser Gln 365	1104
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 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
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ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata gtg 144  
 Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val  
 35 40 45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60

gaa atc tgt gga cat aaa att ata ggt aca gta tta ata gga aat aca 240  
 Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Asn Thr  
 65 70 75 80

cct gcc aac gta att gga aga aat ctg ttg act cag ctt ggt tgc act 288  
 Pro Ala Asn Val Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

gcc ata aag aaa aag gac agt act aaa tgg aga aaa gta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe  
 165 170 175

aga gaa ctt aac aag aga act caa gac ttc tgg gag gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cac ccc gca ggg ata aaa aag aat aaa tca gta act gta cta 624  
 Ile Pro His Pro Ala Gly Ile Lys Lys Asn Lys Ser Val Thr Val Leu  
 195 200 205

gat gta ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg  
 210 215 220

aaa tat act gca ttc acc ata cct agt att aac aat gag aca cca ggg 720

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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
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Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Ile	Lys	Ile	Xaa	Glu	Leu	
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Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
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Lys	Trp	Thr	Val	Gln	Pro	Ile	Thr	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
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gtc	aat	gac	ata	cag	aag	tta	gtg	ggg	aaa	ttg	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
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Ile	Tyr	Ala	Gly													
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Ala	Ile	Lys	Ile	Gly	
1				5					10					15		
ggg	caa	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gtc	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	
			35				40					45				

gga att gga ggt ttt atc aaa gta aag cag tat gat cag gta ctt gta Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Leu Val	192
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gaa att tgt gga cat ara gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Xaa Ala Ile Gly Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgt act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	288
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
100 105 110	
cca ggt atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Ile Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	
gcc ata aag aaa aaa gac agt acc aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	528
165 170 175	
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180 185 190	
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195 200 205	
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210 215 220	
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245 250 255	
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260 265 270	
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275 280 285	
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290 295 300	
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305 310 315 320	



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aga gaa ctt aat aag aga act caa gac ttc tgg gaa gta caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220			672
aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agc agc atg aca aaa att tta gaa cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864
gga tct gac tta raa ata gag cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Xaa Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa cag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Gln Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
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<211> 1116

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 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 57

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1 5 10 15	
ggg caa cta atg gaa gtt cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Met Glu Val Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
rta gaa gaa ata agt tta cca gga aga tgg aaa cca aaa atg ata ggg	144
Xaa Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt gtc aaa gta aaa cag tat gat cag gta ccc tta	192
Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Asp Gln Val Pro Leu	
50 55 60	
gaa att tgt gga aaa aag gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly Lys Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ttt ttg gct cag att ggt tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Phe Leu Ala Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttc ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aag aac agt act aga tgg aga aaa tta gta gat ttt	528
Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag agg acs caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Xaa Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aar aag aac aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg	720





gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ctc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile	
50 55 60	
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag atc ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aga gtt aar caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cca gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca ata atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Ile Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata aag ctg cca gac aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Asp Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat gca gga	1116
Ile Tyr Ala Gly	
370	
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<223> Portion of HIV Reverse Transcriptase	
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1 5 10 15	
ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa ata aat ttg cca ggg aaa tgg aaa cca maa atg ata ggg	144
Leu Glu Glu Ile Asn Leu Pro Gly Lys Trp Lys Pro Xaa Met Ile Gly	
35 40 45	
gga att gga ggt ttt att aaa gta aga cag tat gat caa ata gcc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile	
50 55 60	
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta rta gaa atc tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	

130	135	140	
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gcm ata aag aaa aaa Xaa Ile Lys Lys Lys 165	gac agt act aaa tgg Asp Ser Thr Lys Trp 170	aga aaa tta gta gat ttc Arg Lys Leu Val Asp Phe 175	528
aga gaa ctt aat aag Arg Glu Leu Asn Lys 180	aga act caa gac ttc Arg Thr Gln Asp Phe 185	tgg gaa gtc caa tta gga Trp Glu Val Gln Leu Gly 190	576
ata cca cat ccc gca Ile Pro His Pro Ala 195	ggg tta aaa aag aaa Gly Leu Lys Lys Lys 200	tca gta aca gta cta Ser Val Thr Val Leu 205	624
gat gtg ggt gat gca Asp Val Gly Asp Ala 210	tat ttc tca gtt ccc Tyr Phe Ser Val Pro 215	tta gac caa gac ttc Leu Asp Gln Asp Phe 220	672
aag tat act gca ttt Lys Tyr Thr Ala Phe 225	acc ata cct agt ata Thr Ile Pro Ser Ile 230	aac aat gag aca cca Asn Asn Glu Thr Pro 235	720
att aga tat cag tac Ile Arg Tyr Gln Tyr 245	aat gtg ctt cca cag Asn Val Leu Pro Gln 250	gga tgg aaa gga tca Gly Trp Lys Gly Ser 255	768
gca ata ttc caa agt Ala Ile Phe Gln Ser 260	agc atg aca agg atc Ser Met Thr Arg Ile 265	tta gar cct ttt aga Leu Glu Pro Phe Arg 270	816
caa aat cca gaa ata Gln Asn Pro Glu Ile 275	gtc aty tat cag tac Val Xaa Tyr Gln Tyr 280	atg gat gat tta tat Met Asp Asp Leu Tyr 285	864
gga tct gac tta gaa Gly Ser Asp Leu Glu 290	ata ggg cag cat aga Ile Gly Gln His Arg 295	aca aaa gta gag gaa Thr Lys Val Glu Glu 300	912
aga caa cat ctg ttg Arg Gln His Leu Leu 305	agr tgg ggg ttt tmc Xaa Trp Gly Phe Xaa 310	acg cca gac aaa aag Thr Pro Asp Lys Lys 315	960
cag aaa gaa cct cca Gln Lys Glu Pro Pro 325	ttc ctt tgg atg ggt Phe Leu Trp Met Gly 330	tat gaa ctc cat cct Tyr Glu Leu His Pro 335	1008
aaa tgg aca gta cag Lys Trp Thr Val Gln 340	act ata gaa ctg cca Thr Ile Glu Leu Pro 345	gaa aaa gat agc tgg Glu Lys Asp Ser Trp 350	1056
gtc aat gac ata cag Val Asn Asp Ile Gln 355	aag tta gtg gga aaa Lys Leu Val Gly Lys 360	ttg aat tgg gca agt Leu Asn Trp Ala Ser 365	1104
ata tac cca ggg Ile Tyr Pro Gly 370			1116

<210> 60  
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[illegible][illegible][illegible]



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gaa att tgt gga cat aag gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr 85 90 95	288
tta aat ttt ccc atc agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile ggg Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt cag tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa agc ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Ser Phe Arg 210 215 220	672
aag tac act gca ttt acc ata ccc agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
rca aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa atg gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gag ata gag caa cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960

cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat	1008
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325 330 335	
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
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Ile Tyr Pro Gly	
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1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga caa tat gat cag ata gcc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile	
50 55 60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg atg act cag att ggc tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	



[illegible]

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<221> CDS  
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gga cag cta acg gaa gct yta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly  
 35 40 45

ggr att gga ggt ttt atc aaa gta aga cag tat gat cac gta ctt gta 192  
 Xaa Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp His Val Leu Val  
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat ttg atg act cag ctt ggg ttc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr  
 85 90 95

tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg mca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Xaa Glu Glu  
 115 120 125

aaa ata aaa gca cta aca gaa att tgt aca gaa ttg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly  
 130 135 140

aaa att tca aga ata ggg cct gaa aat cca tac aat act cca ata ttt 480  
 Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe  
 145 150 155 160

gcc ata aag aag aaa aac ggt ayt agg tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asn Gly Xaa Arg Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gag cta aat aag aga act caa gac ttc tgg gaa gtt caa cta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat cct gca gga cta aaa aag aac aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta cat gaa gac ttt aga 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu His Glu Asp Phe Arg  
 210 215 220

aag tat acc gca ttc acc ata cct agt aca aac aat gaa aca cca gga 720

000111-50660260

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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
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gca	ata	ttc	caa	agt	agc	atg	acc	aaa	atc	tta	gaa	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gaa	atg	gtt	atc	tat	caa	tac	gtg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Glu	Met	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
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Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Ile	Lys	Ile	Glu	Glu	Leu	
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Arg	Glu	His	Leu	Leu	Lys	Trp	Gly	Phe	Phe	Thr	Pro	Asp	Glu	Lys	His	
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Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gtg	cag	cct	ata	aaa	ctg	cca	gaa	aaa	gaa	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Lys	Leu	Pro	Glu	Lys	Glu	Ser	Trp	Thr	
			340					345					350			
gtc	aat	gat	ata	cag	aag	tta	gtg	gga	aaa	tta	aat	tgg	gca	agc	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
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att	tat	cca	gga													1116
Ile	Tyr	Pro	Gly													
		370														
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<221>	CDS															
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<223>	Portion of HIV Reverse Transcriptase															
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Ile	Val	Thr	Ile	Lys	Ile	Gly	
	1			5					10					15		
ggg	caa	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	aat	tta	cca	gga	aaa	tgg	aaa	cca	aaa	atr	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Lys	Trp	Lys	Pro	Lys	Xaa	Ile	Gly	
		35					40					45				

gga att gga ggy ttt rtc aaa gta aga cag tat gat cag ata syc ata	192
Gly Ile Gly Xaa Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile	
50 55 60	
gaa atc tgc gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gyc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act	288
Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta caa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Gln Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aag ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gct ata aag aaa aag gac agt gct aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Ala Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cck cat ccc gca ggg ttr aaa aag aaa aaa tca gta aca gta cta	624
Ile Xaa His Pro Ala Gly Xaa Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gta ggt gat gca tat ttt tca gtt ccc tta gat caa aac ttc aga	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asn Phe Arg	
210 215 220	
aag tat act gca ttc acc ata cct agt ata aac aat gag ayg cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gar ata rtt atc tat caa tac gtg gat gat ttg tat gta	864
Gln Asn Pro Glu Ile Xaa Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac ttr gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Xaa Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ytg ttg aag tgg gga ttt acc aca cca gac aag aag cat	960
Arg Gln His Xaa Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	



000111"50660260

130	135	140	
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gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctr Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Xaa 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220			672
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
rtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gac ata att atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Ile Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285			864
gga tct gat ttg gaa ata gag cag cat aga aca aaa ata gag gaa cta Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga gaa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata aag ytg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Xaa Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tat cca ggg Ile Tyr Pro Gly 370			1116

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 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 66

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Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gak rca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Xaa Xaa Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta agr car tat gac cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgt gga cag aaa gct ata ggt aca gta tta gta gga cct acm	240
Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Val Gly Pro Xaa	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gca gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Ala Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt aat ara tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Asn Xaa Trp Arg Lys Leu Val Asp Phe	
165 170 175	
agg gaa ctc aat aag aga act caa gac ttc tgg gaa gtt caa tta ggc	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca rta ctr	624
Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Xaa Xaa	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aar tat act gca ttt acc ata cct agt aca wac aat gag aca cca ggg	720

Lys 225	Tyr	Thr	Ala	Phe	Thr 230	Ile	Pro	Ser	Thr 235	Xaa	Asn	Glu	Thr	Pro	Gly 240		
att Ile	aga Arg	tat Tyr	cag Gln	krc Xaa 245	aat Asn	gtg Val	yyt Xaa	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tcm Xaa 255	cca Pro	768	
gca Ala	ata Ile	ttc Phe 260	mam Xaa 260	agt Ser	agc Ser	ayg Xaa	aca Thr	aaa Lys 265	att Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816	
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tgt Cys 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864	
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ttg Leu	912	
agg Arg 305	caa Gln	cat His	ttg Leu	ttg Leu	agg Arg 310	tgg Trp	ggr Xaa	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	ara Xaa	aaa Lys	cat His 320	960	
cag Gln	aaa Lys	gag Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008	
aaa Lys	tgg Trp	aca Thr 340	gta Val	cag Gln	cct Pro	ata Ile	aaa Lys	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gay Asp	agc Ser 350	tgg Trp	act Thr	1056	
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104	
att Ile	tat Tyr	gca Ala 370	ggg Gly													1116	
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<223> Portion of HIV Reverse Transcriptase																	
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cct Pro 1	caa Gln	atc Ile	act Thr	ctt Leu 5	tgg Trp	caa Gln	cga Arg	cca Pro	ata Ile 10	gtc Val	aca Thr	ata Ile	aag Lys	ata Ile 15	ggg Gly	48	
ggg Gly	caa Gln	cta Leu	aag Lys 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96	
cta Leu	gaa Glu	gaa Glu 35	atg Met	aat Asn	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	ggg Gly	144	



gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata tcc ata Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile 50 55 60	192
gaa atc tgt ggg cat aaa gtt aca ggt aca gtg tta ata gga cct aca Glu Ile Cys Gly His Lys Val Thr Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca ttg gta gaa att tgt gca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Met Glu Lys Glu Gly 130 135 140	432
caa att tca aaa att gag cct gaa aat cca tac aat aat cca gta ttt Gln Ile Ser Lys Ile Glu Pro Glu Asn Pro Tyr Asn Asn Pro Val Phe 145 150 155 160	480
gtc ata aag aaa aaa gac ggt act aac tgg aga aaa tta ata gat ytc Val Ile Lys Lys Lys Asp Gly Thr Asn Trp Arg Lys Leu Ile Asp Xaa 165 170 175	528
aga gaa ctt aat aag aga act caa gat ttc tgg gaa att caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aat aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca ttt tat tca gtt ccc tta gat gag aac ttc agg Asp Val Gly Asp Ala Phe Tyr Ser Val Pro Leu Asp Glu Asn Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca atg gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
aac aat cca gac ata gtc atc tat caa tac atg gat gat ttg tat gta Asn Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gca tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat cta ttr aag tgg gga ttt acc aca cca gac aar aar yat Arg Glu His Leu Xaa Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys Xaa 305 310 315 320	960

cag aaa gaa cct cca ytc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Xaa Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat cca ggg att	1119
Ile Tyr Pro Gly Ile	
370	
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1 5 10 15	
gga caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca ggg aaa tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga atc gga gga ttt atc aaa gta aga cag tat gag cag ata cac ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile His Ile	
50 55 60	
gaa atc tgt ggg cat aaa gct ata ggt aca gtr tta ata gga ccc aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggc tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	

130	135	140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtt ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat cct gca ggg ttg aag aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa aac ttt agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asn Phe Arg 210 215 220			672
aag tat act gca ttt acc ata cct agt ata aat aat gaa aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa gct agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gac atg rtt att tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Met Xaa Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864
ggc tct gac tta gaa ata gga cag cat aga aca aaa ata gaa gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg agg tgg ggg ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctc tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
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<210> 69

<211> 1119

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>  
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 <223> HIV Protease

<221> CDS  
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 <223> Portion of HIV Reverse Transcriptase

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 1 5 10 15

ggg caa yta aag gaa gct mta tta gay aca gga gca gat gat aca gtg 96  
 Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aga gag tat gag cag ata caa gta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Glu Tyr Glu Gln Ile Gln Val  
 50 55 60

gaa atc tgt gga cat aag gct ata rgt aca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Xaa Thr Val Leu Ile Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga aga aat cta atg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gag act gta ccg gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggt cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly  
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat acy ccr gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Xaa Val Phe  
 145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata ccg cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctr 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Xaa  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg  
 210 215 220

aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca gga 720

09709905-1100



gga att gga ggt ttt atc aaa gta aaa cag tat gat cag gta arc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Xaa Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aay ctg ttg aca cag att ggt tgy act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca ara gty aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Xaa Xaa Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aar gca tta atg gaa att tgt gca gay atg gaa aag gaa ggr Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Asp Met Glu Lys Glu Xaa 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
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aga gaa ctt aat aag aaa act caa gac ttt tgg gaa gtc caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccy gca ggg tta aaa aag aac aaa tca gta aca gta ttg Ile Pro His Xaa Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccy tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg 210 215 220	672
aaa tay act gca ttt acm ata cct agt ata aat aat gca aca cca ggg Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Ala Thr Pro Gly 225 230 235 240	720
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cag aat cca gac ata gtt atc tat caa tac atg gat gay ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa mta ggg cag cat aga rca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tta agg tgg ggg ttt acc acw cca gac aag aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Xaa Pro Asp Lys Lys His 305 310 315 320	960

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta car ccc ata gtg ttg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
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Ile Tyr Xaa Gly Ile	
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ggg gca aat aaa gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val	
35 40 45	
gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca	240
Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu	
115 120 125	
aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga	432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly	

130	135	140	
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gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg 210 215 220			672
aar tat act gca ttt acc ata cct agt acg aat aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat ccc gac ata gtt atc tat caa tac gtg gat gat ttg ctt gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Leu Val 275 280 285			864
gga tct gac tta gaa ata gag cag cat aga aca aaa ata gag gag cta Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gcw agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Xaa Ser Gln 355 360 365			1104
att tat cca ggg att Ile Tyr Pro Gly Ile 370			1119

<210> 72

<211> 1119

<212> DNA

<213> Human Immunodeficiency Virus (HIV)



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Lys 225	Tyr	Thr	Ala	Phe	Thr 230	Ile	Pro	Ser	Ile	Asn 235	Glu	Thr	Pro	Gly 240		
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gcm	ata	ttc	caa	tgt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Xaa	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gaa	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Glu	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
ggg	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	cga	cat	ctg	ttg	aag	tgg	gga	ttt	tac	aca	cca	gac	aaa	aaa	cat	960
Arg	Arg	His	Leu	Leu	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
305					310				315						320	
cag	aaa	gaa	ccc	cca	ttc	ctt	tgg	atg	ggt	tat	gag	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
			325						330					335		
aaa	tgg	aca	gta	caa	cct	ata	gtg	cta	cca	gag	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340				345					350				
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aag	tta	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
		355				360						365				
ata	tac	gca	ggg	att												1119
Ile	Tyr	Ala	Gly	Ile												
	370															
<p>&lt;210&gt; 73</p> <p>&lt;211&gt; 1119</p> <p>&lt;212&gt; DNA</p> <p>&lt;213&gt; Human Immunodeficiency Virus (HIV)</p> <p>&lt;220&gt;</p> <p>&lt;221&gt; CDS</p> <p>&lt;222&gt; (0)...(297)</p> <p>&lt;223&gt; HIV Protease</p> <p>&lt;221&gt; CDS</p> <p>&lt;222&gt; (298)...(1119)</p> <p>&lt;223&gt; Portion of HIV Reverse Transcriptase</p> <p>&lt;400&gt; 73</p>																
cct	caa	atc	act	ctt	tgg	caa	cga	ccc	ttc	gtc	aca	gta	aag	ata	ggg	48
Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Phe	Val	Thr	Val	Lys	Ile	Gly	
1				5					10					15		
ggg	cag	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	aat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asn	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	aat	tta	ccg	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	

gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Ile 50 55 60	192
gaa atc tgt gga cac aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga gat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg cct gaa aat cca tac aat acc cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gct ata aag aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gcg ggg tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt ccc cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
cag aat cca gac ata gtt atc tac caa tac gtg gat gac ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gat gag ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Asp Glu Leu 290 295 300	912
agg caa cat ctg ttg aag tgg gga ttt tac aca cca gac aaa aag cat Arg Gln His Leu Leu Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320	960

cag aaa gaa cca cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
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Ile Tyr Pro Gly Ile	
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gag gaa cta aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Leu Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa ata tgt gga cat aaa gct att ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aac ttg ttg act cag ctt ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	

[illegible]

- 121 -

**BOOKS RECEIVED**

- 122 -

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Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Ala		
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ggg																819	
Gly																	
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<223> Portion of HIV Reverse Transcriptase																	
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Asp	Gly	Pro	Lys	Xaa	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Arg		
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Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser		
		35					40					45					
aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gtg	ttt	gct	ata	aag	192	
Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	Ala	Ile	Lys		
	50				55						60						
aaa	aaa	gac	agt	act	aar	tgg	aga	aaa	ttg	gta	gat	ttc	aga	gaa	ctt	240	
Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu		
	65				70				75					80			
aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	ata	cca	cat	288	
Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His		
				85					90					95			
ccc	tca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	gat	gtg	ggg	336	
Pro	Ser	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	Asp	Val	Gly		
			100					105					110				
gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	aag	tat	act	384	
Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	Lys	Tyr	Thr		
		115					120					125					
gca	ttt	act	atn	cct	agt	ata	aac	aat	gag	aca	cca	ggg	att	agg	tat	432	
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cag	tac	aat	gtg	ctt	cca	caa	gga	tgg	aaa	gga	tca	cca	gca	ata	ttc	480	
Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe		
	145				150				155					160			
caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	caa	aat	cca	528	
Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro		
				165				170						175			

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Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val Gly Ser Asp	
180 185 190	
cta gaa ata gga cag cat aga aca aaa ata gag gaa ctg aga cag cat	624
Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His	
195 200 205	
ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat cag aaa gaa	672
Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu	
210 215 220	
cct ccc ttt ctt tgg atg ggc tat gaa ctc cat cct gat aaa tgg aca	720
Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr	
225 230 235 240	
gta cag cct ata gag ctg cca gac aag gat agc tgg act gtc aat gac	768
Val Gln Pro Ile Glu Leu Pro Asp Lys Asp Ser Trp Thr Val Asn Asp	
245 250 255	
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Gly	
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1 5 10 15	
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Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
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Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata cct ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
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Glu Ile Cys Gly His Lys Ala Val Gly Lys Val Leu Val Gly Pro Thr	
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cct gtc aac ata att gga aga aat ctg ttg act caa ctt ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	



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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
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Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
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Ala	Ile	Lys	Lys	Lys	Asn	Ser	Thr	Arg	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Xaa	Xaa	
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Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
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Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
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Lys	Tyr	Thr	Ala	Phe		Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
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Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
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Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
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Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	

355	ata tat gca ggg ile Tyr Ala Gly 370	360		365		1116
<p>&lt;210&gt; 78          &lt;211&gt; 1122          &lt;212&gt; DNA          &lt;213&gt; Human Immunodeficiency Virus (HIV)</p> <p>&lt;220&gt;          &lt;221&gt; CDS          &lt;222&gt; (0)...(297)          &lt;223&gt; HIV Protease</p> <p>&lt;221&gt; CDS          &lt;222&gt; (298)...(1122)          &lt;223&gt; Portion of HIV Reverse Transcriptase</p> <p>&lt;400&gt; 78</p>						
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	ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30					96
	tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45					144
	gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60					192
	gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80					240
	cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Thr Gln Leu Gly Cys Thr 85 90 95					288
	tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110					336
	cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125					384
	aaa ata aaa gca ttg gta gaa ata tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140					432
	aaa att tca aaa att ggg cct gaa aat cca tac aat acr cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Pro Val Phe 145 150 155 160					480
	gcc ata arg aaa aaa gaa agc tct agc tct aaa tgg aga aaa tta gta Ala Ile Xaa Lys Lys Glu Ser Ser Ser Ser Lys Trp Arg Lys Leu Val 165 170 175					528
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<222> (0)...(297)
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<221> CDS
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<223> Portion of HIV Reverse Transcriptase

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Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asn	Thr	Val	
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Phe	Glu	Asp	Leu	Asp	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	
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Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Lys	Gln	Tyr	Glu	Gln	Ile	Pro	Ile	
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Glu	Ile	Cys	Gly	Arg	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
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Pro	Val	Asn	Ile	Ile	Gly	Arg	Asp	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
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cta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
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Pro	Gly	Met	Asp	Gly	Pro	Arg	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
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Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Ala	Glu	Met	Glu	Lys	Glu	Gly	
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Ala	Ile	Lys	Lys	Lys	Asn	Ser	Asn	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
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Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Ile	Thr	Val	Leu	
		195					200					205				
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Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	
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Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
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		290				295					300						
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Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	Leu	Thr	Thr	Pro	Asp	Gln	Lys	His		
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Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
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Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Asp	Lys	Asp	Ser	Trp	Thr		
			340				345						350				
gtc	aat	gac	ata	cag	aag	tta	gtg	ggr	aaa	ttg	aat	tgg	gca	agt	caa		1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Xaa	Lys	Leu	Asn	Trp	Ala	Ser	Gln		
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Ile	Tyr	Pro	Gly														
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Thr	Ile	Lys	Ile	Gly		
1				5					10					15			
ggg	cag	cta	aag	gag	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta		96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val		
			20					25					30				
tta	gaa	gaa	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg		144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro						

**SECRET**

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gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528				
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ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	ggg Gly	ttg Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624				
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aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	ggg Gly 240	720				
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1119

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 Gly Gln Leu Xaa Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
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 Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggt ttt atc aaa gta aaa cag tat gat caa ata ccy rta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Xaa Xaa  
 50 55 60  
 gaa att tgt gga cat aga gct ata ggt aca gtw tta gta gga cct aca 240  
 Glu Ile Cys Gly His Arg Ala Ile Gly Thr Xaa Leu Val Gly Pro Thr  
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 Pro Val Asn Ile Ile Gly Xaa Asn Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95  
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140  
 aaa att tca aga att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gct ata aag aaa aar gat agt act aaa tgg aga aaa tta gta gat ttc 528  
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ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val  
20 25 30

tta gaa gaa atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg 144  
Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta 192  
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val  
50 55 60

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Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
65 70 75 80

ccc gtc aac ata att gga aga aat ctg ttg act cag att ggg tgc act 288  
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432  
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
130 135 140

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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
145 150 155 160

gcc ata aaa aag aaa gac agt act aaa tgg aga aag tta gta gat ttc 528  
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165 170 175

aga gaa ctt aay aaa aag act caa gac ttc tgg gaa gtt caa tta gga 576  
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
180 185 190

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Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
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Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Xaa Phe Arg  
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly  
225 230 235 240

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Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
245 250 255

gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816  
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Gln Asn Pro Asp Ile Val Ile	Tyr Gln Tyr Met Asp	Asp Leu Tyr Val	
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Gly Ser Asp Leu Glu Ile Xaa Lys His Arg Thr Lys Ile Glu Glu Leu			
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Gln Lys Glu Pro Pro Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp			
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Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr			
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Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
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Leu Glu Asp Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly			
35	40	45	
gga att gga ggt ttt atc aaa gta aga cag tat gat caa gta ccc ata			192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile			
50	55	60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca			240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr			
65	70	75	80
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act			288

Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr	
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tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
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Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
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Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
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Val	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
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Ala	Tyr	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
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Lys	Trp	Thr	Val	Gln	Pro	Ile	Xaa	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			



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ggg Gly																	
caa Gln	cta Leu	aag Lys 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96		
tta Leu																	
gaa Glu	gaa Glu 35	atg Met	aat Asn	ttg Leu	cca Pro	ggg Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	ggg Gly	144		
gga Gly																	
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gaa Glu 65																	
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tta Leu																	
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cca Pro																	
gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aga Arg	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384		
aaa Lys																	
ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu 140	atg Met	gag Glu	aag Lys	gaa Glu	ggr Xaa	432		
aaa Lys 145																	
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gtg Val 210	ggg Gly	gat Asp	gcr Xaa	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccy Xaa	tta Leu 220	gay Asp	aaa Lys	gay Asp	ttc Phe	agg Arg	672		
aag Lys 225																	
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gca Ala																	
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Gly Ser Asp Leu Glu Ile	Gln His Arg Thr Lys Ile	Glu Glu Leu	
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cag aaa gaa cct cca ttc ctt	tgg atg ggg tat gaa ctc	cat ccg gat	1008
Gln Lys Glu Pro Pro Phe Leu	Trp Met Gly Tyr Glu Leu	His Pro Asp	
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gtm aat gac ata cag aar tta	gta gga aaa ttg aat tgg	gcg agt cag	1104
Xaa Asn Asp Ile Gln Lys Leu	Val Gly Lys Leu Asn Trp	Ala Ser Gln	
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ggg cac aca acg gaa gct cta	tta gat aca gga gca gat gat	aca gta	96
Gly His Thr Thr Glu Ala Leu	Leu Asp Thr Gly Ala Asp Asp	Thr Val	
20	25	30	
tta gaa gaa atg aat ttg cca	ggg aga tgg aaa cca aaa atg	ata gga	144
Leu Glu Glu Met Asn Leu Pro	Gly Arg Trp Lys Pro Lys Met	Ile Gly	
35	40	45	
gga att gga ggt ttt atc aaa	gta aga cag tat gag cag gta	ccc ata	192
Gly Ile Gly Gly Phe Ile Lys	Val Arg Gln Tyr Glu Gln Val	Pro Ile	
50	55	60	
gaa ttc tgt gga cat aaa act	gta ggt aca gta tta ata gga	cct aca	240
Glu Phe Cys Gly His Lys Thr	Val Gly Thr Val Leu Ile Gly	Pro Thr	
65	70	75	80
cct gtc aac ata att gga	aga aat ctg atg act cag att	ggt tgt act	288

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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
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cca	gga	atg	gat	ggg	ccc	aaa	gtt	aaa	cca	tgg	cca	ttg	aca	gaa	aga	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Pro	Trp	Pro	Leu	Thr	Glu	Arg	
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Lys	Asn	Lys	Ala	Leu	Val	Glu	Ile	Cys	Ser	Glu	Met	Glu	Lys	Gly	Arg	
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Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu	
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Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Glu	Phe	Arg	
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aag	tat	act	gca	ttc	acc	ata	cct	agt	aca	aac	aat	gaa	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Thr	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttc	caa	tgt	agc	atg	aca	aaa	atc	tta	gag	ccc	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gaa	ata	gtt	atc	tgt	cag	tac	atg	gat	gac	ttg	tat	gta	864
Gln	Asn	Pro	Glu	Ile	Val	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gca	tct	gat	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	gta	gag	gaa	ctg	912
Ala	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Val	Glu	Glu	Leu	
	290					295					300					
aga	caa	cat	ctg	ttg	aag	tgg	ggg	ttt	ttc	aca	cca	gac	gaa	aaa	cat	960
Arg	Gln	His	Leu	Leu	Lys	Trp	Gly	Phe	Phe	Thr	Pro	Asp	Glu	Lys	His	
	305				310				315						320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gta	cag	cct	ata	gta	ctg	cca	gac	caa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Asp	Gln	Asp	Ser	Trp	Thr	
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1           5           10           15

ggg caa cta agg raa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Arg Xaa Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
           20           25           30

tta gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
           35           40           45

gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
           50           55           60

gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
           65           70           75           80

cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt tgc act      288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr
           85           90           95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
           100          105          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu
           115          120          125

aaa ata gaa gca tta atr gaa att tgt gma ttt ttg gaa aag gaa gga      432
Lys Ile Glu Ala Leu Xaa Glu Ile Cys Xaa Phe Leu Glu Lys Glu Gly
           130          135          140

aaa att tca aaa att ggg cct gaa aat ccg tac aac act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
           145          150          155          160

gcc ata aag aaa aaa gga ggt act aaa tgg aga aaa ata gta gat ttc      528
Ala Ile Lys Lys Lys Gly Gly Thr Lys Trp Arg Lys Ile Val Asp Phe
           165          170          175

aga gaa ctt aat aaa aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
           180          185          190

ata cca cat ccc gcg ggg tta aaa aag aay aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
           195          200          205

gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ctc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Leu Arg
           210          215          220

aag tat act gca ttt act ata cct agt aca aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly
           225          230          235          240

att aga tac caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
           245          250          255

gca ata ttt caa agt agc atg aca aaa atc tta gag ccc ttt aga aag      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys

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Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	ccc	atc	agt	cct	att	gaa	cct	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Pro	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	ctg	gaa	aaa	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Leu	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	ata	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Ile	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctg	aat	aag	aaa	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	acg	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aaa	tat	act	gca	ttt	acc	ata	cct	agt	aca	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Thr	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gca	ata	ttt	caa	cat	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	His	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
cag	aat	cca	gac	ata	gtt	atc	tat	caa	tac	gtg	gat	gac	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	gaa	cat	ctg	ttg	aag	tgg	gga	ttt	tac	aca	cca	gac	aaa	aaa	cat	960
Arg	Glu	His	Leu	Leu	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
	305				310					315					320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			

gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
 Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln  
           355                          360                          365

att tat gca ggg 1116  
 Ile Tyr Ala Gly  
           370

<210> 90  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

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           1                          5                          10                          15

gga cag cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val  
                           20                          25                          30

tta gaa gaa atg aac ttg cca gga aaa tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly  
                           35                          40                          45

gga att gga ggt ttt gtc aga gta aga caa tat gat cag gta cct gta 192  
 Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Asp Gln Val Pro Val  
           50                          55                          60

gaa att tgt gga cat aaa gct ata ggt tca gta tta gta gga cca aca 240  
 Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr  
           65                          70                          75                          80

cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt ttc act 288  
 Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr  
                           85                          90                          95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
                           100                          105                          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
                           115                          120                          125

aaa ata aaa gca tta gta gar att tgt aca gaa ytg gaa aaa gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Xaa Glu Lys Glu Gly  
           130                          135                          140

aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
           145                          150                          155                          160

gcc ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Leu Val Asp Phe  
                           165                          170                          175







00011"50650260

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gga tct gac cta gaa ata ggg Gly Ser Asp Leu Glu Ile Gly 290 295	cag cat aga aca aaa Gln His Arg Thr Lys 300	ata gag gaa ctg Ile Glu Glu Leu	912
aga caa cat ttg ttg aaa tgg Arg Gln His Leu Leu Lys Trp 305 310	gga ttt atc aca cca Gly Phe Ile Thr Pro 315	gat gaa aaa cat Asp Glu Lys His 320	960
cag aaa gaa cct cca ttc ctt Gln Lys Glu Pro Pro Phe Leu 325	tgg atg ggg tat gaa ctc Trp Met Gly Tyr Glu Leu 330	cat cct gat His Pro Asp 335	1008
aag tgg aca gta cag cct ata Lys Trp Thr Val Gln Pro Ile 340	gta ctg cca gaa aaa Val Leu Pro Glu Lys 345	gac agc tgg act Asp Ser Trp Thr 350	1056
gtc aat gac ata cag aaa tta Val Asn Asp Ile Gln Lys Leu 355	gtg gga aaa ttg aat Val Gly Lys Leu Asn 360 365	tgga gca agt cag Trp Ala Ser Gln	1104
att tat gca gg Ile Tyr Ala 370			1115
<p>&lt;210&gt; 92            &lt;211&gt; 1116            &lt;212&gt; DNA            &lt;213&gt; Human Immunodeficiency Virus (HIV)</p>			
<p>&lt;220&gt;            &lt;221&gt; CDS            &lt;222&gt; (0)...(297)            &lt;223&gt; HIV Protease</p>			
<p>&lt;221&gt; CDS            &lt;222&gt; (298)...(1116)            &lt;223&gt; Portion of HIV Reverse Transcriptase</p>			
<p>&lt;400&gt; 92</p>			
cct cag atc act ctt tgg caa cga ccc ctc Pro Gln Ile Thr Leu Trp Gln Arg Pro 1 5 10	gtc aca ata aag ata ggg Val Thr Ile Lys Ile Gly 15		48
ggg cag cta aag gaa gct cta tta Gly Gln Leu Lys Glu Ala Leu Leu 20 25	gat aca gga gca gat gat aca gta Thr Gly Ala Asp Asp Thr Val 25 30		96
tta gaa gac ata aac ttg cca gga Leu Glu Asp Ile Asn Leu Pro Gly 35 40	aaa tgg aaa cca aaa atg ata ggg Lys Trp Lys Pro Lys Met Ile Gly 45		144
gga att gga ggt ttt atc aaa gta Gly Ile Gly Gly Phe Ile Lys Val 50 55	aga cag tat gag cag gta ccc ata Arg Gln Tyr Glu Gln Val Pro Ile 60		192
gaa atc tgt gga cat aaa act ata Glu Ile Cys Gly His Lys Thr Ile 65 70	ggt aca gta tta gta gga cct aca Gly Thr Val Leu Val Gly Pro Thr 75 80		240
cct gtc aac ata att gga aga aat ctg atg act cag att ggg tgc act			288

Pro	Val	Asn	Ile	Ile 85	Gly	Arg	Asn	Leu	Met 90	Thr	Gln	Ile	Gly	Cys 95	Thr	
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	ggg Gly	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	aac Asn	agt Ser	act Thr	aga Arg	tgg Trp 170	aga Arg	aaa Lys	gta Val	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aaa Lys	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	ggg Gly	tta Leu	aaa Lys 200	aag Lys	aac Asn	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	gaa Glu	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	acg Thr	cca Pro	ggg Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	ata Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ctg Leu	gtt Val	atc Ile	tgt Cys 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	tta Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	cta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gaa Glu	gaa Glu	ctg Leu	912
agg Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	gaa Glu	aaa Lys	cat His 320	960
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gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag 1104  
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355 360 365

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Ile Tyr Ala Gly

1116

370

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<210> 93
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<212> DNA
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<220>
<221> CDS
<222> (0) ... (297)
<223> HIV Protease
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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata gga      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
  1           5           10           15
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ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gta 96  
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val  
20 25 30

tta gaa gaa atg aat tta cca gga aga tgg aca cca aaa ata ata ggg 144  
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Thr Pro Lys Ile Ile Gly  
35 40 45

gga att gga ggt ttt gtc aga gta aga cag tat gaa cag ata ccc gta 192  
Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Glu Gln Ile Pro Val  
50 55 60

gaa atc tgc ggg cat aaa gct gta ggt aca gta tta gta gga cct aca 240  
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr  
65 70 75 80

cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgt act 288  
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
85 90 95

tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aag 336  
Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys  
100 105 110

cga gga atg gat ggc cca ara gtt aaa caa tgg cca ttg aca gaa gag 384  
Pro Gly Met Asp Gly Pro Xaa Val Lys Gln Trp Pro Leu Thr Glu Glu  
115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gam gga 432  
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Xaa Gly  
130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
145 150 155 160

gct ata aag aaa aaa gac agt act aaa tgg aga aaa gta gta gat ttc 528  
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165 170 175

[illegible]

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<210> 94
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<220>
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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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 1 5 10 15  
  
 ggg caa cta ata gag gct cta ttg gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val  
 20 25 30  
  
 tta gaa gaa atg gat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144  
 Leu Glu Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly  
 35 40 45  
  
 gga att gga ggt tgg atc aaa gta aga caa tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Trp Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60  
  
 gaa att tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr  
 65 70 75 80  
  
 cca gtc aac gta att gga aga aat ctg atg act cag att ggt tgc act 288  
 Pro Val Asn Val Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr  
 85 90 95  
  
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 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
  
 cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
  
 aag ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gat ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly  
 130 135 140  
  
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
  
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa gta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe  
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 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190  
  
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 Ile Pro His Pro Ala Gly Leu Pro Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205  
  
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 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg  
 210 215 220  
  
 aaa tat act gca ttt acc ata cct agt ata aat aat gag aca cca gga 720  
 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly  
 225 230 235 240  
  
 gtt aga tat cag tac aat gtg ctc cca cag ggg tgg aaa gga tca cca 768  
 Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
 245 250 255  
  
 gca ata ttc caa agt agc atg acc aaa atc tta gag cct ttt aga aaa 816  
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	260		265		270	
cag aat cca aac ata ctt att tgt caa tac atg gat gat ttg tat gta						864
Gln Asn Pro Asn Ile Leu Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val						
275			280		285	
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg						912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu						
290			295		300	
aga caa cat ctg tgg aga tgg ggg ttt tac aca cca gat aaa aaa cat						960
Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His						
305			310		315	320
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat						1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp						
			325		330	335
aaa tgg aca gta cag cct ata gag ctg cca gaa aaa gac agc tgg act						1056
Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr						
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Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Xaa Gln						
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Ile Tyr Ala Gly						
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Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val						
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Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly						
35 40 45						
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Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ser Val						
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Glu Ile Cys Xaa His Lys Ala Ile Gly Thr Val Leu Xaa Gly Pro Thr						
65 70 75 80						
cct gtc aac ata att gga agg aat ttg ttg act cag att ggt tgc act						288

Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
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Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
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Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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aga	gaa	ctt	aat	aag	aaa	act	caa	gac	ttt	tgg	gar	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195				200						205				
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Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
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Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
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Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
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Gln	Asn	Pro	Glu	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
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Gly	Ser	Asp	Leu	Glu	Ile	Glu	Gln	His	Arg	Ile	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
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Arg	His	His	Leu	Leu	Lys	Trp	Gly	Phe	Xaa	Thr	Pro	Asp	Lys	Lys	His	
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cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
			325						330					335		
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Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			

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att tac cca ggg 1116  
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ggg caa cta agg gaa gct cta tta gat aca gga gca gat gat aca gta 96  
Gly Gln Leu Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val  
20 25 30

tta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144  
Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly  
35 40 45

gga att ggg ggt ttt atc aaa gta aga sag tat gat cag gta ccc gta 192  
Gly Ile Gly Gly Phe Ile Lys Val Arg Xaa Tyr Asp Gln Val Pro Val  
50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga ccc aca 240  
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta ara tta aag 336  
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Xaa Leu Lys  
100 105 110

cca ggr atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
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115 120 125

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Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
130 135 140

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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe  
145 150 155 160

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165 170 175





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Gly Gln Ile Lys Glu Xaa Leu Leu Asp Thr Gly Ala Asp Asp Thr Val  
20 25 30

tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa ttg ata ggg 144  
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Leu Ile Gly  
35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt ata 192  
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile  
50 55 60

gaa atc tgt ggc cat aaa gct ata ggt aca gta tta gta gga cct aca 240  
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr  
65 70 75 80

cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288  
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
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115 120 125

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Lys Ile Lys Ala Leu Leu Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly  
130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480  
Lys Ile Ser Lys Ile Ile Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
165 170 175

aga gaa ctt aat aag aga act caa gac ttt tgg gag gtt caa cta gga 576  
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
180 185 190

ata cca cat ccc gsa ggg tta aga aag aaa aaa tca gta aca gta ctg 624  
Ile Pro His Pro Xaa Gly Leu Arg Lys Lys Lys Ser Val Thr Val Leu  
195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gag gac tty agg 672  
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg  
210 215 220

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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly  
225 230 235 240

att agg tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca 768  
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro  
245 250 255

gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa 816  
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys

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aga caa cat ctg tgg cag tgg Arg Gln His Leu Trp Gln Trp Gly 305 310	ttt ttc aca cca gac Phe Phe Thr Pro Asp 315	aaa aaa cat Lys Lys His 320	960
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gtc aat gac ata cag aag tta gtg Val Asn Asp Ile Gln Lys Leu Val 355 360	gga aaa ttg aat tgg gca agt cag Gly Lys Leu Asn Trp Ala Ser Gln 365		1104
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ggg caa cta aag gaa gct cta tta gat Gly Gln Leu Lys Glu Ala Leu Leu Asp 20 25	aca gga gca gat gat aca gta Thr Gly Ala Asp Thr Val		96
tta gaa gaa atg cat ttg cca gga Leu Glu Glu Met His Leu Pro Gly 35 40	aaa tgg aaa cca aaa atg ata ggg Lys Trp Lys Pro Lys Met Ile Gly 45		144
gga att gga ggt ttt atc aaa gta Gly Ile Gly Gly Phe Ile Lys Val 50 55	aga cag tat gat cag ata cct gta Arg Gln Tyr Asp Gln Ile Pro Val 60		192
gaa aty tgt gga cat aaa gct ata Glu Xaa Cys Gly His Lys Ala Ile 65 70	ggt aca gta tta gta gga cct aca Thr Val Leu Val Gly Pro Thr 75 80		240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act			288

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cca Pro	ggg Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
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ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gga Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tac Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	ggg Gly 240	720
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aga Arg 305	caa Gln	cac His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	ggr Xaa	ttt Phe	acc Thr	ack Xaa 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
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aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
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Ile Pro His Pro Ser Gly Leu Xaa Lys Lys Lys Ser Val Thr Val Leu
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gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gat ttc agg      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg
      210                               215                               220

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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
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      245                               250                               255

gca ata ttc caa agc agc atg aca aaa atc tta gag cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys
      260                               265                               270

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      275                               280                               285

rgc tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg      912
Xaa Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu
      290                               295                               300

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His
      305                               310                               315                               320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
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aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act      1056
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      340                               345                               350

gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
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att tat gca gg
Ile Tyr Ala
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<220>
<221> CDS
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<223> HIV Protease

<221> CDS
<222> (298)...(1115)
<223> Portion of HIV Reverse Transcriptase

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ggg	cag	ctr	aag	gaa	gct	ata	tta	gat	aca	gga	gca	gat	gat	aca	kta		96
Gly	Gln	Xaa	Lys	Glu	Ala	Ile	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Xaa		
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tta	gaa	gaa	atg	aat	tng	ccc	gga	aga	tgg	ama	cca	ama	ttg	ata	ggg		144
Leu	Glu	Glu	Met	Asn	Xaa	Pro	Gly	Arg	Trp	Xaa	Pro	Xaa	Leu	Ile	Gly		
			35				40					45					
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Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile		
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Glu	Ile	Cys	Gly	His	Lys	Val	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr		
	65				70					75					80		
cct	acc	aac	ata	att	gga	aga	aat	ctg	atg	act	cag	ctt	ggt	tgc	act		288
Pro	Thr	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Met	Thr	Gln	Leu	Gly	Cys	Thr		
				85					90					95			
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag		336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
			100					105					110				
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa		384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
		115					120					125					
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	ttg	gaa	aag	gaa	ggg		432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Leu	Glu	Lys	Glu	Gly		
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Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
					150					155					160		
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc		528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe		
				165					170					175			
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga		576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
			180					185					190				
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	ata	ctg		624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Ile	Leu	</	

	260	265	270	
	caa aat cca gac ata gtt atc tat	caa tac gtg gat gat	ttg tat gta	864
	Gln Asn Pro Asp Ile Val Ile Tyr	Gln Tyr Val Asp Asp	Leu Tyr Val	
	275	280	285	
	gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg			912
	Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu			
	290	295	300	
	aga caa cat ctg tgg agg tgg gga ttt tac aca cca gac aaa aaa cat			960
	Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His			
	305	310	315	320
	cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat			1008
	Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
	325	330	335	
	aaa tgg aca gta cag cct ata arg ttg cca gaa aaa gac agc tgg act			1056
	Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr			
	340	345	350	
	gtc aat gam ata cag aaa tta gtg gga aaa tta aat tgg gcc agt cag			1104
	Val Asn Xaa Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln			
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	Ile Xaa Xaa			
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	ggr cag yta aag gaa gct tta tta gay aca gra gca gat gat mca gta			96
	Xaa Gln Xaa Lys Glu Ala Leu Leu Asp Thr Xaa Ala Asp Asp Xaa Val			
	20	25	30	
	tta gaa gaa atg tat ttg cca gga aga tgg aaa cca aaa atg ata ggg			144
	Leu Glu Glu Met Tyr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly			
	35	40	45	
	gga att gga ggt ttt atc aag gta aga cag tat gat cag ata ccc ata			192
	Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile			
	50	55	60	
	gaa atc tgt gga cac aaa gct ata ggt aca gta ttg gta gga tct aca			240
	Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr			
	65	70	75	80
	cct gtt aac ata att gga aga aat ctg ttg act cag att ggt tgc acc			288





gtc aat gac ata cag aag tta gta gga aaa ttg aat tgg g 1096  
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp  
355 360 365

<210> 102  
<211> 1048  
<212> DNA  
<213> Human Immunodeficiency Virus (HIV)

<220>  
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<223> HIV Protease

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<223> Portion of HIV Reverse Transcriptase

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1 5 10 15  
ggg caa cta aag gaa gct cta ttg gat aca gga gca gat gat aca ata 96  
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile  
20 25 30  
tta gaa gaa atg tgt ttg cca gga aga tgg aaa cca aaa ttg ata ggg 144  
Leu Glu Glu Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly  
35 40 45  
gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata 192  
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
50 55 60  
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca 240  
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr  
65 70 75 80  
cct gcc aac ata gtt gga aga aat ctg ttg act cag att ggc tgt act 288  
Pro Ala Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr  
85 90 95  
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
100 105 110  
cca gga atg gat ggg cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
115 120 125  
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gag aag gat gga 432  
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly  
130 135 140  
aaa att tca aaa att ggg cct gaa aat cca tay aat act cca gta ttt 480  
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
145 150 155 160  
gcc ata aag aaa aaa aat agt gat aaa tgg aga aaa gta gta gat ttc 528  
Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Val Val Asp Phe  
165 170 175  
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga 576  
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
180 185 190

ata cca cat ccc gga ggg tta rag aag aac aaa tca ata aca gta ctg	624
Ile Pro His Pro Gly Gly Leu Xaa Lys Asn Lys Ser Ile Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc aga	672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata ccy agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Xaa Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tat aat gtg ctt cca cag gga tgg aag gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gcc ata ttc caa agt agc atg aca aaa ata tta gag cct ttt aga aag	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata att atc gtt caa tac gtg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Ile Ile Val Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gca tct gac tta gaa ata ggg cag cat aga aca aaa ata aag gaa cta	912
Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Lys Glu Leu	
290 295 300	
aga caa tat ctg tgg gag tgg gga ttt tac aca cca gac aaa aaa cat	960
Arg Gln Tyr Leu Trp Glu Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	
305 310 315 320	
caa cag gaa ccc cca ttc ctc tgg atg ggg tat gag ctc cat cct gat	1008
Gln Gln Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac a	1048
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp	
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1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	

35					40					45						
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	cag	ata	ccc	ata	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile	
	50					55					60					
gaa	atc	tgt	gga	cat	aaa	gct	gaa	ggt	aca	gta	tta	gta	gga	cct	aca	240
Glu	Ile	Cys	Gly	His	Lys	Ala	Glu	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
	65				70				75						80	
ccg	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	att	ggt	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85				90						95		
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ctg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	aba	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	ggr	432
Lys	Ile	Lys	Ala	Leu	Xaa	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Xaa	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	ccg	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aaa	act	caa	gac	ttt	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cac	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gaa	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Glu	Phe	Arg	
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aag	tat	aca	gca	ttt	acc	ata	cct	agt	aca	aac	aat	gag	aca	ccc	agg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Thr	Asn	Asn	Glu	Thr	Pro	Arg	
	225				230					235					240	
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tat	gtg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gag	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	saa	cat	ctg	ttg	agg	tgg	gga	ttt	acc	aca	cca	gac	aaa	aaa	cat	960

Arg	Xaa	His	Leu	Leu	Arg	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His		
305					310					315					320		
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008	
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
				325					330					335			
aaa	tgg	aca	gtr	cag	cct	ata	rag	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056	
Lys	Trp	Thr	Xaa	Gln	Pro	Ile	Xaa	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr		
			340					345					350				
gtc	aat	gac	ata	cag	aaa	tta	gtg	gga	aaa	tta	aat	tgg	gca	agt	cag	1104	
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln		
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Ile	Tyr	Ala	Gly														
			370														
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1				5					10					15			
ggg	caa	tta	aaa	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96	
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val		
			20					25					30				
cta	gaa	gaa	ata	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg	144	
Leu	Glu	Glu	Ile	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly		
			35				40					45					
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	car	ata	cyt	ata	192	
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Xaa	Ile		
	50				55						60						
gaa	atc	tgt	gga	cat	aaa	gct	ata	ggg	aca	gta	tta	gta	gga	cct	aca	240	
Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr		
	65				70				75					80			
cct	gtc	aac	ata	att	gga	aga	aat	ctg	ttr	act	cag	att	ggc	tgc	act	288	
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Xaa	Thr	Gln	Ile	Gly	Cys	Thr		
				85				90					95				
tta	aat	ttt	ccc	ata	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336	
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
			100					105					110				
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384	
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
		115					120					125					



<212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
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 <223> HIV Protease

<221> CDS  
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 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat aat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val  
 20 25 30

ttt gaa gac ytg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144  
 Phe Glu Asp Xaa Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly  
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ctt gta 192  
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Leu Val  
 50 55 60

gaa atc tgt gga caa aaa gct ata ggt aca gta tta ata gga cct aca 240  
 Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr  
 65 70 75 80

cct gtc aac ata att gga agg gat ctg ttg act cag att ggt tgc act 288  
 Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr  
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly  
 130 135 140

aar att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160

gcc ata aag aaa aaa gac agt act aar tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gay ttc agg 672  
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg

210	215	220	
aag tat act gca ttt acc ata cct agc ata aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa tgt agc atg aca aaa atc tta gat cct ttt aga aag Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270			816
caa aat cca gac cta gtt atc tat caa tac rtg gat gac ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Tyr Val 275 280 285			864
gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga car cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aar cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tac cca ggg Ile Tyr Pro Gly 370			1116

<210> 106  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 106 cct cag atc act ctt ngg caa cga ccm att gtc aca ata aag gta ggg Pro Gln Ile Thr Leu Xaa Gln Arg Xaa Ile Val Thr Ile Lys Val Gly 1 5 10 15	48
ggg cam tta aaa gaa gtt ytt tta gat mma gga gca gat gat cma gta Gly Xaa Leu Lys Glu Val Xaa Leu Asp Xaa Gly Ala Asp Asp Xaa Val 20 25 30	96
tta gaa gaa atr gat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144



Leu	Glu	Glu	Xaa	Asp	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	
		35					40					45				
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	caa	ata	gtt	gta	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Val	Val	
	50					55					60					
gaa	atc	tgt	gga	cat	aaa	gct	ata	ggt	aca	gta	tta	gta	gga	cct	aca	240
Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
	65				70					75					80	
cct	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	ctt	ggt	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gag	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	ttg	gta	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	aty	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Xaa	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
agg	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	yta	aaa	aag	aac	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Xaa	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu	
			195				200					205				
gat	gtg	ggt	gat	gca	tat	ttc	tca	gtt	ccc	tta	gat	aaa	gac	ttt	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aag	tat	act	gca	ttt	acc	ata	ccc	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
att	aga	tat	cag	tat	aat	gtg	ctt	cca	caa	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	cta	gag	cct	ttt	agg	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gaa	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					

aga gca cat ctg tta aag tgg gga ttt acc aca cca gay aaa aag cat	960
Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gtg cag cct ata aag ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gcc agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat cca gga	1116
Ile Tyr Pro Gly	
370	

<210> 107  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease  
  
 <221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

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Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg caa cta aag gaa gct tta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta agm cag tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa att tgt gga cat aaa gct gtg ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act aag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Lys Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	

[illegible]

<210> 108

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 <220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease  
  
 <221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 108	
cct caa atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gtg	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca ggg aaa tgg aag cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggg ttt atc aaa gta agm crg tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Xaa Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgt gra cat aaa gct aya ggt aca gta tta ata ggm cct act	240
Glu Ile Cys Xaa His Lys Ala Xaa Gly Thr Val Leu Ile Xaa Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga awt ctg atg act cag att ggg tgc act	288
Pro Val Asn Ile Ile Gly Arg Xaa Leu Met Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cct gca ggt tta aaa aag aaa aaa tca gta aca gta cta	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggg gat gca tat ttt tca gtt ccc tta gat gaa aac ttc agg	672

[illegible]

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<210> 109
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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ttg Leu	gam Xaa	gaa Glu 35	ata Ile	aat Asn	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	ggg Gly	144
gga Gly	att Ile 50	gra Xaa	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aam Xaa	cag Gln	tat Tyr	gat Asp 60	sag Xaa	ata Ile	mcc Xaa	ata Ile	192
gac Asp 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gta Val	ata Ile	ggt Gly	aca Thr	ata Ile 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	gat Asp	ctg Leu 90	ttg Leu	act Thr	cag Gln	att Ile	ggc Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gar Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu 140	ttg Leu	gaa Glu	aag Lys	gaa Glu	gga Gly	432
aag Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aac Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aag Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	cct Pro	gca Ala	ggg Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	tty Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gmt Xaa 220	aaa Lys	gaa Glu	tnn Xaa	nnn Xaa	672
nnn Xaa 225	nnn Xaa	nnn Xaa	nnn Xaa	nnn Xaa	nnn Xaa 230	nnn Xaa	nnn Xaa	nnn Xaa	nnn Xaa	nnn Xaa 235	nnn Xaa	nnn Xaa	nnn Xaa	nnn Xaa	nnn Xaa 240	720
nnn Xaa	nnn Xaa	nnn Xaa	nnn Xaa	nnn Xaa 245	nnn Xaa	nnn Xaa	nnn Xaa	cca Pro	cag Gln	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gaa Glu	ata Ile	gtt Val	atc Ile	tac Tyr 280	car Gln	tac Tyr	rtg Xaa	gat Asp	gay Asp 285	ttg Leu	ttw Xaa	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912

aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggy tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat cca ggg	1116
Ile Tyr Pro Gly	
370	
<210> 110	
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<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
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1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atr aat ttg cca ggr aaa tgg aaa cca awa atg ata ggg	144
Leu Glu Glu Xaa Asn Leu Pro Xaa Lys Trp Lys Pro Xaa Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile	
50 55 60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca ggg atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	

115	120	125	
aaa ata aaa gca tta ata gaa atc tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140			432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gtg aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220			672
aag tac act gca ttt mcc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa mat cca gac atg gty atc tat caa tac atg gat gat ttg tat gta Gln Xaa Pro Asp Met Xaa Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864
gga tct gac tta gaa ata ggr cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Xaa Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300			912
aga cag cat ttg ttg aag tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gag ctg cca gaa aar gam agc tgg act Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Xaa Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aaa ata gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Ile Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tac cca ggg Ile Tyr Pro Gly 370			1116



<210> 111  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)  
  
 <220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease  
  
 <221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

<400> 111	
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1 5 10 15	
ggg caa ata aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Ile Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val	
20 25 30	
tta gaa gaa atg agc ttg cca gga aaa tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta agm cag tat gwt cat ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Xaa His Ile Pro Ile	
50 55 60	
gaa wtc tgt ggm cat aaa gct gaa ggt aca gta tta ata gga cct aca	240
Glu Xaa Cys Xaa His Lys Ala Glu Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc ata agt cct att gaa act gta cca gta aga cta aaa	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Arg Leu Lys	
100 105 110	
cca gga atg gat ggg cca aaa gtt aag caa tgg cca cta aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa atc aaa gca ttg ata gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att gaa aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Glu Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata agg aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Arg Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttt tgg gaa att caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	

gat	gtg	ggg	gat	gca	tat	ttt	tca	ggt	ccc	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
210						215					220					
aag	tat	act	gca	ttt	acc	ata	cct	agt	gta	aat	aat	gag	aca	cca	gga	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Val	Asn	Asn	Glu	Thr	Pro	Gly	
225					230					235					240	
att	aga	tat	caa	tac	aat	gtg	ctt	cca	caa	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gaa	yta	gtt	atc	tac	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Glu	Xaa	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tca	gac	tta	gaa	ata	gar	aag	cat	aga	gca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Glu	Lys	His	Arg	Ala	Lys	Ile	Glu	Glu	Leu	
		290				295						300				
aga	gaa	cat	ctg	tya	aaa	tgg	ggg	ttt	acc	aca	cca	gac	aaa	aaa	cat	960
Arg	Glu	His	Leu	Xaa	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	
305					310				315						320	
cag	aaa	gaa	cct	cca	ttt	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gta	cag	acc	ata	aag	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Thr	Ile	Lys	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			
gtc	aat	gat	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agt	caa	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
		355					360					365				
att	tat	cca	ggg													1116
Ile	Tyr	Pro	Gly													
		370														

<210> 112  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1116)  
 <223> Portion of HIV Reverse Transcriptase

cct	cag	atc	act	ctt	tgg	caa	cga	ccc	ctc	gtc	aca	ata	aag	ata	ggg	48
Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Thr	Ile	Lys	Ile	Gly	
1				5				10						15		
ggg	cag	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atk ata ggg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Xaa Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtc aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta atg gaa att tgt gca gaa wtg gaa aag gaa gga Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Glu Xaa Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agc act aaa tgg ara aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Xaa Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aar aga act caa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag acm cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	912



Pro	Gly	Met	Asp	Gly	Pro	Arg	Val	Lys	Gln	Trp	Pro	Leu	Xaa	Glu	Glu		
		115					120					125					
aaa	ata	aaa	gca	tta	ata	gaa	atc	tgc	aca	gaa	atg	gaa	aag	gam	sga	432	
Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Xaa	Xaa		
	130					135					140						
waa	att	tca	aaa	mta	ggg	cct	gam	wat	cca	tac	aat	act	cca	gta	ttt	480	
Xaa	Ile	Ser	Lys	Xaa	Gly	Pro	Xaa	Xaa	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
	145				150					155					160		
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528	
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe		
				165					170					175			
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576	
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
			180					185					190				
ata	cca	cac	ccg	gca	ggg	tta	aaa	aag	aac	aaa	tca	gta	aca	gtg	ttg	624	
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu		
		195					200					205					
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gag	ttc	agg	672	
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Glu	Phe	Arg		
	210					215					220						
aag	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720	
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly		
	225				230					235					240		
atc	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768	
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro		
			245						250					255			
gca	ata	ttc	caa	tst	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816	
Ala	Ile	Phe	Gln	Xaa	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys		
			260					265					270				
caa	aat	cca	gaa	ata	gtt	atc	tgt	caa	tac	atg	gat	gat	ttg	tat	gta	864	
Gln	Asn	Pro	Glu	Ile	Val	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val		
		275					280					285					
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ttg	912	
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu		
	290					295					300						
aga	gaa	cat	ctg	ttg	aag	tgg	gga	ttt	acc	aca	cca	gat	aaa	aaa	cat	960	
Arg	Glu	His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His		
	305				310				315						320		
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gag	ctc	cat	cct	gat	1008	
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
			325						330					335			
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056	
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr		
			340					345					350				
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agt	cag	1104	
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln		
		355					360					365					
att	tat	gca	ggg													1116	
Ile	Tyr	Ala	Gly														
	370																

0970695 1300

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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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- 186 -

gac gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt tcy ata cct agt aca aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	
225 230 235 240	
agt agg tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ser Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg ata aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Ile Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca raa att gtg atc tat cma tac mtg gat gat ttg tat gta	864
Gln Asn Pro Xaa Ile Val Ile Tyr Xaa Tyr Xaa Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aar gaa cct ccg ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac ags ttg rct	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Xaa Leu Xaa	
340 345 350	
kca aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tac tca ggg	1116
Ile Tyr Ser Gly	
370	

<210> 115  
 <211> 1116  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0) ... (297)  
 <223> HIV Protease

<221> CDS  
 <222> (298) ... (1116)  
 <223> Portion of HIV Reverse Transcriptase

cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gtg	96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	

ttg	gaa	gaa	atg	agt	ata	cca	gga	aaa	tgg	aaa	cca	aaa	ttg	ata	ggg	144		
Leu	Glu	Glu	Met	Ser	Ile	Pro	Gly	Lys	Trp	Lys	Pro	Lys	Leu	Ile	Gly			
35																40	45	
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	cag	gkg	ccc	gta	192		
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Xaa	Pro	Val			
50																55	60	
gaa	att	tgt	gga	cat	aaa	gct	ata	ggt	mca	gtw	tta	ata	ggm	cct	aca	240		
Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	Xaa	Xaa	Leu	Ile	Xaa	Pro	Thr			
65																70	75	80
cct	gcc	aac	ata	att	gga	agg	aat	ctg	ttg	act	cag	att	ggt	tgc	act	288		
Pro	Ala	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr			
85																90	95	
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336		
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys			
100																105	110	
cca	gga	atg	gat	ggc	cca	aaa	gtt	aag	caa	tgg	cca	ttg	aca	gaa	gag	384		
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu			
115																120	125	
aaa	ata	aaa	gca	tta	aca	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga	432		
Lys	Ile	Lys	Ala	Leu	Thr	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly			
130																135	140	
aag	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480		
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe			
145																150	155	160
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528		
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe			
165																170	175	
aga	gaa	ctt	aat	aag	aga	act	caa	gat	ttc	tgg	gaa	gtt	caa	tta	gga	576		
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly			
180																185	190	
ata	cca	cat	cct	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624		
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu			
195																200	205	
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	gaa	gac	ttt	agg	672		
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg			
210																215	220	
aaa	tat	act	gca	ttt	acc	ata	cct	agt	gta	aac	aat	gag	aca	cca	ggg	720		
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Val	Asn	Asn	Glu	Thr	Pro	Gly			
225																230	235	240
att	aga	tat	cag	tat	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768		
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro			
245																250	255	
gca	ata	ttc	caa	tgt	agt	atg	aca	aaa	ata	tta	gag	ccc	ttt	aga	aaa	816		
Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys			
260																265	270	
caa	aat	cca	gac	cta	gtt	atc	tat	caa	tac	gtg	gat	gat	ttg	tat	gta	864		
Gln	Asn	Pro	Asp	Leu	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val			
275																280	285	
gga	tct	gac	tta	gaa	ata	ggg	cag</											



290	295	300	
aga caa cat ctg ttg aaa tgg ggt ttt acc aca cca gac aaa aag cat			960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His			
305	310	315	320
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat			1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
	325	330	335
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act			1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			
	340	345	350
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag			1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln			
	355	360	365
att tac cca ggg			1116
Ile Tyr Pro Gly			
370			
<210> 116			
<211> 1116			
<212> DNA			
<213> Human Immunodeficiency Virus (HIV)			
<220>			
<221> CDS			
<222> (0)...(297)			
<223> HIV Protease			
<221> CDS			
<222> (298)...(1116)			
<223> Portion of HIV Reverse Transcriptase			
<400> 116			
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg			48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly			
1	5	10	15
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gac aca gta			96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
	20	25	30
tta gaa gaa ata agt ctg cca gga aga tgg aaa cca aaa ttg ata ggg			144
Leu Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly			
	35	40	45
gga att gga ggt ttt atc aaa gta aag cag tat gat cag ata ccc ata			192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile			
	50	55	60
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta ggm cct aca			240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr			
	65	70	75
cct gtc aac ata gtt gga aga aat ctg ttg act cag ctt ggt tgc act			288
Pro Val Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr			
	85	90	95
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
	100	105	110
cca gga atg gat ggc cca aag gtt aag caa tgg cca ttg aca gaa gaa			384

[illegible]

<210> 117  
 <211> 1119  
 <212> DNA  
 <213> Human Immunodeficiency Virus (HIV)

<220>  
 <221> CDS  
 <222> (0)...(297)  
 <223> HIV Protease

<221> CDS  
 <222> (298)...(1119)  
 <223> Portion of HIV Reverse Transcriptase

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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly  
 1 5 10 15  
 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96  
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val  
 20 25 30  
 tta gaa gaa atg gat ttg cca gga aga tgg aca cca aaa atg ata ggg 144  
 Leu Glu Glu Met Asp Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly  
 35 40 45  
 gga att gga ggt ctt gtc aaa gta aga cag tat gat cag ata ccc ata 192  
 Gly Ile Gly Gly Leu Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile  
 50 55 60  
 gaa atc tgt gga cat aaa act ata ggt aca gta tta gta gga cct aca 240  
 Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr  
 65 70 75 80  
 cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgt act 288  
 Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr  
 85 90 95  
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336  
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys  
 100 105 110  
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384  
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu  
 115 120 125  
 aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga 432  
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly  
 130 135 140  
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt 480  
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe  
 145 150 155 160  
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528  
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe  
 165 170 175  
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576  
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly  
 180 185 190  
 ata cca cat cct gca gga tta aaa aag aaa aaa tca gta aca gta ctg 624  
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu  
 195 200 205

gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gac	aag	gac	ttt	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aaa	tat	act	gca	ttt	acc	ata	cct	agt	aca	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Thr	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gca	ata	ttc	caa	agc	agc	atg	aca	aaa	atc	tta	gat	cct	ttt	aga	aag	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Asp	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tgt	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	gaa	cat	ctg	tgg	aag	tgg	ggg	ttt	tac	aca	cca	gac	aaa	aaa	cat	960
Arg	Glu	His	Leu	Trp	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
	305				310				315						320	
cag	aaa	gaa	cct	ccg	ttc	ctc	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325				330						335		
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340				345					350				
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aac	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
		355					360					365				
att	tat	yca	ggg	att												1119
Ile	Tyr	Xaa	Gly	Ile												
	370															

&lt;210&gt; 118

&lt;211&gt; 979

&lt;212&gt; PRT

&lt;213&gt; Human Immunodeficiency Virus

&lt;400&gt; 118

Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	Pro	Gly	Met
1				5					10					15	
Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys
			20					25					30		
Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser
		35					40					45			
Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Ile	Phe	Ala	Ile	Lys
	50					55				60					
Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu
65					70					75				80	
Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His
				85				90					95		
Pro	Ala	Gly	Leu	Lys	Gln	Lys	Lys	Ser	Val	Thr	Ile	Leu	Asp	Val	Gly
			100					105					110		
Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Gly	Phe	Arg	Lys	Tyr	Thr
		115					120					125			

Ala	Phe	Thr	Ile	Pro	Ser	Arg	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr
130						135					140				
Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe
145					150					155					160
Gln	Ser	Ser	Met	Thr	Arg	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro
				165					170					175	
Glu	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	Asp
			180					185					190		
Leu	Glu	Ile	Gly	Gln	His	Arg	Ala	Lys	Ile	Glu	Glu	Leu	Arg	Gly	His
	195						200					205			
Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys	Glu
210					215						220				
Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	Trp	Thr
225					230					235					240
Val	Gln	Pro	Ile	Lys	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn	Asp
				245					250					255	
Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Ala
			260					265					270		
Gly	Ile	Lys	Val	Arg	Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala
	275						280					285			
Leu	Thr	Glu	Val	Ile	Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala
290						295					300				
Glu	Asn	Arg	Glu	Ile	Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr	Asp
305					310					315					320
Pro	Ser	Lys	Asp	Leu	Ile	Ala	Glu	Ile	Gln	Lys	Gln	Gly	Gln	Gly	Gln
				325					330					335	
Trp	Thr	Tyr	Gln	Ile	Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu	Lys	Thr	Gly
			340					345					350		
Lys	Tyr	Ala	Arg	Met	Arg	Gly	Ala	His	Thr	Asn	Asp	Val	Lys	Gln	Leu
		355					360					365			
Thr	Glu	Ala	Val	Gln	Lys	Ile	Thr	Thr	Glu	Ser	Ile	Val	Ile	Trp	Gly
	370					375					380				
Lys	Thr	Pro	Lys	Phe	Lys	Leu	Pro	Ile	Gln	Lys	Glu	Thr	Trp	Glu	Thr
385					390					395					400
Trp	Trp	Thr	Glu	Tyr	Trp	Gln	Ala	Thr	Trp	Ile	Pro	Glu	Trp	Glu	Phe
				405					410					415	
Val	Asn	Thr	Pro	Pro	Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu	Lys	Glu
			420					425					430		
Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr	Val	Asp	Gly	Ala	Ala	Asn	Arg
		435					440					445			
Glu	Thr	Lys	Leu	Gly	Lys	Ala	Gly	Tyr	Val	Thr	Asn	Arg	Gly	Arg	Gln
	450					455					460				
Lys	Val	Val	Thr	Leu	Thr	Asp	Thr	Thr	Asn	Gln	Lys	Thr	Glu	Leu	Gln
465					470					475					480
Ala	Ile	Tyr	Leu	Ala	Leu	Gln	Asp	Ser	Gly	Leu	Glu	Val	Asn	Ile	Val
				485					490					495	
Thr	Asp	Ser	Gln	Tyr	Ala	Leu	Gly	Ile	Gln	Ala	Gln	Pro	Asp	Gln	
			500					505					510		
Ser	Glu	Ser	Glu	Leu	Val	Asn	Gln	Ile	Ile	Glu	Gln	Leu	Ile	Lys	Lys
		515					520					525			
Glu	Lys	Val	Tyr	Leu	Ala	Trp	Val	Pro	Ala	His	Lys	Gly	Ile	Gly	Ser
	530					535					540				
Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	Pro	Gly	Met	Asp	Gly	Pro
545					550					555					560
Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys	Ala	Leu	Val
				565					570					575	
Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly
			580					585					590		
Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Ile	Phe	Ala	Ile	Lys	Lys	Lys	Asp
		595					600					605			
Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg
	610					615					620				
Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly
625					630					635					640
Leu	Lys	Gln	Lys	Lys	Ser	Val	Thr	Ile	Leu	Asp	Val	Gly	Asp	Ala	Tyr
				645					650					655	
Phe	Ser	Val	Pro	Leu	Asp	Glu	Gly	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr

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Ile	Pro	Ser	660	Arg	Asn	Asn	Glu	Thr	665	Pro	Gly	Ile	Arg	Tyr	670	Gln	Tyr	Asn
Val	Leu	Pro	675	Gln	Gly	Trp	Lys	Gly	680	Ser	Pro	Ala	Ile	Phe	685	Gln	Ser	Ser
Met	Thr	Arg	690	Ile	Leu	Glu	Pro	Phe	695	Arg	Lys	Gln	Asn	Pro	700	Glu	Ile	Val
705						710						715						720
Ile	Tyr	Gln	725	Tyr	Met	Asp	Asp	Leu	730	Tyr	Val	Gly	Ser	Asp	735	Leu	Glu	Ile
Gly	Gln	His	740	Arg	Ala	Lys	Ile	Glu	745	Glu	Leu	Arg	Gly	His	750	Leu	Leu	Lys
Trp	Gly	Phe	755	Thr	Thr	Pro	Asp	Lys	760	Lys	His	Gln	Lys	Glu	765	Pro	Pro	Phe
Leu	Trp	Met	770	Gly	Tyr	Glu	Leu	His	775	Pro	Asp	Lys	Trp	Thr	780	Val	Gln	Pro
Ile	Lys	Leu	785	Pro	Glu	Lys	Asp	Ser	790	Trp	Thr	Val	Asn	Asp	795	Ile	Gln	Lys
Leu	Val	Gly	805	Lys	Leu	Asn	Trp	Ala	810	Ser	Gln	Ile	Tyr	Ala	815	Gly	Ile	Lys
Val	Arg	Gln	820	Leu	Cys	Lys	Leu	Leu	825	Arg	Gly	Thr	Lys	Ala	830	Leu	Thr	Glu
Val	Ile	Pro	835	Leu	Thr	Glu	Glu	Ala	840	Glu	Leu	Glu	Leu	Ala	845	Glu	Asn	Arg
Glu	Ile	Leu	850	Lys	Glu	Pro	Val	His	855	Gly	Val	Tyr	Tyr	Asp	860	Pro	Ser	Lys
Asp	Leu	Ile	865	Ala	Glu	Ile	Gln	Lys	870	Gln	Gly	Gln	Gly	Gln	875	Trp	Thr	Tyr
Gln	Ile	Tyr	885	Gln	Glu	Pro	Phe	Lys	890	Asn	Leu	Lys	Thr	Gly	895	Lys	Tyr	Ala
Arg	Met	Arg	900	Gly	Ala	His	Thr	Asn	905	Asp	Val	Lys	Gln	Leu	910	Thr	Glu	Ala
Val	Gln	Lys	915	Ile	Thr	Thr	Glu	Ser	920	Ile	Val	Ile	Trp	Gly	925	Lys	Thr	Pro
Lys	Phe	Lys	930	Leu	Pro	Ile	Gln	Lys	935	Glu	Thr	Trp	Glu	Thr	940	Trp	Trp	Thr
Glu	Tyr	Trp	945	Gln	Ala	Thr	Trp	Ile	950	Pro	Glu	Trp	Glu	Phe	955	Val	Asn	Thr
Pro	Pro	Leu	965	Val	Lys	Leu	Trp	Tyr	970	Gln	Leu	Glu	Lys	Glu	975	Pro	Ile	Val
Gly	Ala	Glu																